



Sequence Listing

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly
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Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser
				155				160						165

Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu
				170				175						180

His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu
				185				190						195

Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu
				200				205						210

Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50

tgagcttctg gtgccntttg gctctaattc tggccacaca gagaancagt 100

cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150

agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200

tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250

aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300

ggcccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350

tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400

gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcattctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tatcctggtt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttgagaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgagaa ntttgngntg ttcctttgcg gattttctcc 250

tttttccag ttccagtcac agngaggcg catctcaccg gngngntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400
gggaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattccagc tccggtcacg gggagggcgc atntcaccgg gtggctgang 50
aactgaaga aaaccttngt ccttgccccc agntttgtgn tgcggatnat 100
cgctctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcctctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50

gcctgcctgg gagcctgtc cctgtcagc tgcgcgtcct gcctctgcgg 100

ctctgcccc tgcctcctgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt ctctcttttc accctgctca tgctctgct 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
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cctcttcctc ctcatccagc tgggtgctgt catcgacttt gcgcactcct 600
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tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
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gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050
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gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
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 agggctccct tgtctcagg ctccacggga gcggggctgc tggagagagc 1750
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc cccagggga ccctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser
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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro
			20						25					30

Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
			35						40					45

Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
			50						55					60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly
			65						70					75

Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser
			80						85					90

Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala
			95						100					105

Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser
			110						115					120

Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe
			125						130					135

Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr
			140						145					150

Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val
			155						160					165

Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile
			170						175					180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcattcagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttccac ttctgcctgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc acgg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcaccac acg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgtgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgtctctc 100
cgcggcacgt ccgcgaggac ttgaagtctt gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccgga aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
tttaggataa acgtaggcct gcgtggcctg gtggctgggtg gcataattgg 750
agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
 cctccctgag aaaattgaaa gtagttttacg ggaagatgaa cctgagaatg 950
 atgctaagaa aattgaagca ctgctaaacc ttccctagaaa cccttcagta 1000
 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050
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 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
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 t 1351

<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala
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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30
Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val
				35					40					45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu
				50					55					60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala
				65					70					75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val
				80					85					90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile
				95					100					105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val
				110					115					120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly
				125					130					135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 29
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 ctattaccgc gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
 ttcgttcatg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgccct caacctgctt tacaccttg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300
tccgagtggc cggcgtggtc attgcagtgg gcattcttct gtccctgatt 350
gcttttagtg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttgattt tattgttcag tttctgtat 450
cttgccgttg tttagccctg aaccaggagc aacagggtca gcttctggag 500
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550
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cagttttaca gagatccctg gtgtttggct gacctacaga tacaggaacc 750
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taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950
ttttctttcc gttgctgaaa aatatttgaa acttggtggtc tctgaagctc 1000
ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

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 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
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 aaaagatatt tgattatctt aaaaattgtt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
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 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

Met	Val	Cys	Gly	Gly	Phe	Ala	Cys	Ser	Lys	Asn	Cys	Leu	Cys	Ala
1				5					10					15
Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35				40						45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50				55						60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65				70						75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80				85						90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95				100						105

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn
 110 115 120
 Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn
 125 130 135
 Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser
 140 145 150
 Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val
 155 160 165
 Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu
 170 175 180
 Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp
 185 190 195
 Pro Arg Ala Asn Pro Ser Ala Phe Leu
 200

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggtggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300
 gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350
 gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27

<223> unknown base

<400> 38

aatcccaa at tccccaat ttttggnctt tttagggaaa gatgtgttgt 50
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ttacaccaat gtattctaga atagttatgt cttaggaaat tgtgggttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500
ggaggaaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgttttagc ccctgaaacc aggagcaaca gggncagct tcctggaggt 100
tggttgga caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200
tggtctngctg tggtaaaagt gacctcgt gctcgccatg tgctccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
accacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggcccaaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
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gacgtgcag tgtgaggagc ctgtctgcac tgaggagagc agctgccaca 150
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400
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gtccaagaac tgtttccagc gccaatcttc agagctgtac cctcagctga 550
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tgcagaggtc agctgcccgc ctctctttct cttctacaa ggatggaagg 650
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 atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgcctt 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

Met	Lys	Leu	Gly	Cys	Val	Leu	Met	Ala	Trp	Ala	Leu	Tyr	Leu	Ser	1	5	10	15
Leu	Gly	Val	Leu	Trp	Val	Ala	Gln	Met	Leu	Leu	Ala	Ala	Ser	Phe	20	25	30	
Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	35	40	45	
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	50	55	60	
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val	65	70	75	
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe	80	85	90	
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp	95	100	105	
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly	110	115	120	
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys	125	130	135	
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro	140	145	150	
Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195	

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgccacg ggtccgccca cgcgtccggg 50
ccaccagaag tttagcctc tttagtagca ggaggctgga agaaaggaca 100
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gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
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ccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
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gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

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 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
				200					205					210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
				215					220					225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
				230					235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
				245					250					255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
				260					265					270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
				275					280					285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
				290					295					300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
				305					310					315
Val	Tyr	Glu	Ala	Ala	Arg									
				320										

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggcggcgcg 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcggga tgcctcctct 200

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ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaaa aagtggatgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

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<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30

Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45

Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
			50						55					60

Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
			65						70					75

Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
			80						85					90

Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105

Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120

Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125						130				135

Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140						145				150

Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155						160				165

Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
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170	175	180
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185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
350	355	360
Ser Met Ile Pro Ser Gln Ser Arg Ala	Phe Gln Thr Val	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser Arg Asn Gly	Ser Phe Ile Thr Lys	Glu Lys Lys Asp Thr Val
575	580	585
Leu Arg Gln Val	Arg Leu Asp Pro Cys Asp	Leu Gln Pro Ile Phe
590	595	600
Asp Asp Met Leu	His Phe Leu Asn Pro	Glu Glu Leu Arg Val Ile
605	610	615
Glu Glu Ile Pro	Gln Ala Glu Asp Lys	Leu Asp Arg Leu Phe Glu
620	625	630
Ile Ile Gly Val	Lys Ser Gln Glu Ala	Ser Gln Thr Leu Leu Asp
635	640	645
Ser Val Tyr Ser	His Leu Pro Asp Leu	Leu
650	655	

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
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<210> 66
 <211> 24
 <212> DNA
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<220>
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<210> 67
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 acgatgatcg cgggctccct tctctgtgtt ggattcctta gcaccaccac 50

<210> 68
 <211> 2412
 <212> DNA
 <213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

50					55					60				
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly
				65										75
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala
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Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
				95										105
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe
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Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly
				125										135
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr
				140										150
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
				155										165
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
				170										180
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
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Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg
				200										210
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu
				215										225
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His
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Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala
				245										255
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile
				260										270
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His
				275										285
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg
				290										300
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr
				305										315
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
				320										330
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala

335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala		
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr		
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr		
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val		
395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe		
410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg		
425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp		
440	445	450
Leu Lys Thr		

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cggtcaatgc agaaatgac cagcctgtgt gcctgccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly
				20					25					30
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala
				35					40					45
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp
				50					55					60
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu
				65					70					75
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile
				80					85					90
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp
				95					100					105
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly
				110					115					120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgtctgc tcntgagaga 200

gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgcacac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctcaggg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
tacctgcacg atgggcac 18

<210> 79
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<220>
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<400> 79
caactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
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<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
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<400> 83
gtgcaaccaa cagatacaaa ctcttccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

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atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200
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<210> 85

<211> 67

<212> PRT

<213> Homo sapiens

<400> 85

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Leu	Ala	Leu	Leu	Leu	Pro	Val	Gln	Val	Ser	Ser	Phe	Val	Pro	Leu
				20				25					30	

Thr	Ser	Met	Pro	Glu	Ala	Thr	Ala	Ala	Glu	Thr	Thr	Lys	Pro	Ser
				35				40					45	

Asn	Ser	Ala	Leu	Gln	Pro	Thr	Ala	Gly	Leu	Leu	Val	Val	Leu	Leu
				50				55					60	

Ala	Leu	Leu	His	Leu	Tyr	His
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<223> Synthetic oligonucleotide probe

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<210> 87
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<400> 87
ggtagagatg tagaaggga agcaagacc 29

<210> 88
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<212> DNA
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<210> 89
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<212> DNA
<213> Homo sapiens

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 cagctgttga tgccagtgtc ctctaactca tgctgtcctt gtgattaaac 2500
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 cacaacttca gctttgcatt acgagctctg tattccaaga aaatcaaagt 2900
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 ttttaa 2956

<210> 90

<211> 432

<212> PRT

<213> *Homo sapiens*

<400> 90

Met	Pro	Ala	Arg	Pro	Gly	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Arg	Pro
1				5					10					15

Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20					25				30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35					40					45

Ala Asp Gly Pro	Pro	Ala Ala Asp Gly	Glu Asp Gly Gln Asp	Pro	
	50		55	60	
His Ser Lys His	Leu Tyr Thr Ala Asp	Met Phe Thr His Gly	Ile		
	65		70	75	
Gln Ser Ala Ala	His Phe Val Met Phe	Phe Ala Pro Trp Cys	Gly		
	80		85	90	
His Cys Gln Arg	Leu Gln Pro Thr Trp	Asn Asp Leu Gly Asp	Lys		
	95		100	105	
Tyr Asn Ser Met	Glu Asp Ala Lys Val	Tyr Val Ala Lys Val	Asp		
	110		115	120	
Cys Thr Ala His	Ser Asp Val Cys Ser	Ala Gln Gly Val Arg	Gly		
	125		130	135	
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro	Gly Gln Glu Ala Val	Lys		
	140		145	150	
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr	Leu Glu Asn Trp Met	Leu		
	155		160	165	
Gln Thr Leu Asn	Glu Glu Pro Val Thr	Pro Glu Pro Glu Val	Glu		
	170		175	180	
Pro Pro Ser Ala	Pro Glu Leu Lys Gln	Gly Leu Tyr Glu Leu	Ser		
	185		190	195	
Ala Ser Asn Phe	Glu Leu His Val Ala	Gln Gly Asp His Phe	Ile		
	200		205	210	
Lys Phe Phe Ala	Pro Trp Cys Gly His	Cys Lys Ala Leu Ala	Pro		
	215		220	225	
Thr Trp Glu Gln	Leu Ala Leu Gly Leu	Glu His Ser Glu Thr	Val		
	230		235	240	
Lys Ile Gly Lys	Val Asp Cys Thr Gln	His Tyr Glu Leu Cys	Ser		
	245		250	255	
Gly Asn Gln Val	Arg Gly Tyr Pro Thr	Leu Leu Trp Phe Arg	Asp		
	260		265	270	
Gly Lys Lys Val	Asp Gln Tyr Lys Gly	Lys Arg Asp Leu Glu	Ser		
	275		280	285	
Leu Arg Glu Tyr	Val Glu Ser Gln Leu	Gln Arg Thr Glu Thr	Gly		
	290		295	300	
Ala Thr Glu Thr	Val Thr Pro Ser Glu	Ala Pro Val Leu Ala	Ala		
	305		310	315	
Glu Pro Glu Ala	Asp Lys Gly Thr Val	Leu Ala Leu Thr Glu	Asn		
	320		325	330	

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
425 430

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

atgttcttcg cgccctggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtgtcgc cttgtgcaac gtgc 24

<210> 94

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaagg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
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 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn		
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser		
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly		
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys		
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
275		

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

qatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
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catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys	320	325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala	335	340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln	350	355	360
Leu Cys Gly Val	His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro	365	370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met	380	385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly	395	400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His Arg Val Thr Val Phe Gln	410	415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser	425	430	435
Lys Ala Glu Arg	Gly His Lys Val Arg Leu Ala Val Gly Ser Gly	440	445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro	455	460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala	470	475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser	485	490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp	500	505	510
Val Thr Thr Gly	Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met	515	520	525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser	530	535	540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala	545	550	555
Gln Gly Lys Leu	Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe	560	565	570
Phe Asn Thr Gly	Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu	575	580	585
Arg Phe His Asp	Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu	590	595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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<210> 104

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 104

ggagaatgtg gccacaac 18

<210> 105

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
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<400> 106
atccacttca gcggacac 18

<210> 107
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ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

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 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys	20	25	30	
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	35	40	45	
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys	50	55	60	
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	65	70	75	
Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	

Thr Gly Gly Asn	Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu	Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu	Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro	Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala	Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg	Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys	Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly	Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met	Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn	Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly	Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile	Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser	Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala	Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe	Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr	Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu	Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp	Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn	Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met Asn Asp Gly	Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val	Asp
440		445	450
Val Asp Ile Thr	Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile	Met
455		460	465
Ala Leu Arg Val	Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn	Gly
470		475	480
Asn Asp Val Asn	Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly	Ser
485		490	495
Gly Ser Gly Ser	Gly Cys Met Asp Asp	Val Cys Pro Thr Glu	Phe
500		505	510
Glu Phe Val Thr	Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg	Arg
515		520	525
Glu Val Asp Ser	Ser Ala Ala Gln Arg	Gly His Ser Leu Leu	Ser
530		535	540
Trp Ser Leu Thr	Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys	Arg
545		550	555

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

aagcgtgaca gcgggcacgt c 21

<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

<400> 113
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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
tagggaccgc gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200
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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

Met	Ala	Pro	Arg	Gly	Cys	Ala	Gly	His	Pro	Pro	Pro	Pro	Ser	Pro	1	5	10	15
Gln	Ala	Cys	Val	Cys	Pro	Gly	Lys	Met	Leu	Ala	Met	Gly	Ala	Leu	20	25	30	
Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys
155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly
170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr
185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr
200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn
215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln
230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro
245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser
260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile
275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu
290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly
305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly
320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys
335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His
350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val
365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly
380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu
395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His
410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln
425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
 cccaacccaa ctgtttacct ctgg 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
 gccaccctac ctcagaaact gaaggagggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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acagcaaggg agtctgtgaa gctacatgct aacctggatg taagtttggt 350
gagtgcgtgg gaccaaaca atgcagatgc tttccaggat acaccgggaa 400
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cgcccatgcc 450
aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550
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 gtaataataa 2260

<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu	Pro	Leu	Leu	Leu	Ser	Trp
1				5					10					15

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
335

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggtg ctggtgctgt ggcgctgct cctgctcttg 50

gtgcagctgc tgcgttctt gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatgggtg 150

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gcggtacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400
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aatgaaaaac atgaaaacag caatcttctt atgcttctga ataataaag 1100
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gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
				20					25				30	
Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40				45	
Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55				60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggagg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaatg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
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caatcaatcc aacagcatat tcggttgcac cttctacaca ctacagctat 150
tgttaggttg cctgaggaca cgctgggcct ctgtcctgat gctgctgagc 200
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 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser	Leu Met Trp Leu Ser Phe
35	40	45
Arg Lys Val Gln Glu	Pro Gln Gly Lys Ala	Lys Arg His Gly Asn
50	55	60
Thr Val Pro Gly Glu	Trp Pro Trp Gln Ala	Ser Val Arg Arg Gln
65	70	75
Gly Ala His Ile Cys	Ser Gly Ser Leu Val	Ala Asp Thr Trp Val
80	85	90
Leu Thr Ala Ala His	Cys Phe Glu Lys Ala	Ala Ala Thr Glu Leu
95	100	105
Asn Ser Trp Ser Val	Val Leu Gly Ser Leu	Gln Arg Glu Gly Leu
110	115	120
Ser Pro Gly Ala Glu	Glu Val Gly Val Ala	Ala Leu Gln Leu Pro
125	130	135
Arg Ala Tyr Asn His	Tyr Ser Gln Gly Ser	Asp Leu Ala Leu Leu
140	145	150
Gln Leu Ala His Pro	Thr Thr His Thr Pro	Leu Cys Leu Pro Gln
155	160	165
Pro Ala His Arg Phe	Pro Phe Gly Ala Ser	Cys Trp Ala Thr Gly
170	175	180
Trp Asp Gln Asp Thr	Ser Asp Ala Pro Gly	Thr Leu Arg Asn Leu
185	190	195
Arg Leu Arg Leu Ile	Ser Arg Pro Thr Cys	Asn Cys Ile Tyr Asn
200	205	210
Gln Leu His Gln Arg	His Leu Ser Asn Pro	Ala Arg Pro Gly Met
215	220	225
Leu Cys Gly Gly Pro	Gln Pro Gly Val Gln	Gly Pro Cys Gln Gly
230	235	240
Asp Ser Gly Gly Pro	Val Leu Cys Leu Glu	Pro Asp Gly His Trp
245	250	255
Val Gln Ala Gly Ile	Ile Ser Phe Ala Ser	Ser Cys Ala Gln Glu
260	265	270
Asp Ala Pro Val Leu	Leu Thr Asn Thr Ala	Ala His Ser Ser Trp
275	280	285
Leu Gln Ala Arg Val	Gln Gly Ala Ala Phe	Leu Ala Gln Ser Pro
290	295	300
Glu Thr Pro Glu Met	Ser Asp Glu Asp Ser	Cys Val Ala Cys Gly
305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	365	370	375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	380	385	390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	395	400	405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	410	415	420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	425	430	435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	440	445	450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	455	460	465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	470	475	480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	485	490	495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	500	505	510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	515	520	525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	530	535	540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	545	550	555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	560	565	570

Cys

<210> 133
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggcccgcc cgggccccca ttcgggccgg gcctcgctgc ggcggcgact 50
gagccaggct gggccgcgtc cctgagtccc agagtccggc cggcgccggca 100
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gatgctgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200
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gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850
atgccttccg gatgtcatct ctccctgcc caggaatgga agatgtgagg 1900
acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950

atTTTgGgGa aaataaatgt cTTtqtaaaa aaaaaaaaaa aaaaaaaaaa 1998

<211> 316

<213> Hom

 $\langle 221 \rangle$

<222> 233

<223> unk

Met Leu .

1 5 10 15

20 25 30

22

Year	Chl. a	Year	Chl. a	Year	Chl. a	Year	Chl. a	Year	Chl. a	Year	Chl. a	Year	Chl. a	Year	Chl. a
1951	35	1952	40	1953	45	1954	50	1955	55	1956	60	1957	65	1958	70

35 40 45

Ala Thr Leu Cys Cys Ser Phe Ser Phe Glu Phe Gly Phe Ser Leu

50 55 60

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu

65 70 75

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala

00 05 00

Aug Aug Thru Ala Jan Dec Dec Dec Dec Dec Dec Dec Dec Dec Dec Dec Dec Dec

Leu Phe P10 Asp Leu Leu Ala Gln Gly Asn Ala

Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe

Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser

Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Gly

100

170 175 180

185 190 195

200 205 210

215 220 225

215 220 225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
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<210> 139
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 gctgtctgtc tgtctcattg 20

<210> 140
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 140
 agacacagta tactgaccac 20

<210> 141
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgcgaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145
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 Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
 20 25 30
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
 35 40 45
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
 50 55 60
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
 65 70 75
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
 80 85 90
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
 95 100 105
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
 110 115 120
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
 125 130 135
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
 140 145 150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
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Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

qcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgccca ccaggacgga gcatggagggt cacagtacct 250
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 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 gccctgcctt cagcctcagc gggctcagtc tctttttctc tttggtgcc 200
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 gatgtgtcgg tgatgtgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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gaggtnccaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100
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ccctgaactg gatattaccag gagtgcaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350
ctacatcatg aaccccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgccctgcct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

tgcggcgacc gtcgtacacc atgggcctcc acctccgcc ctaccgtgtg 50

gggctgctcc cggatggcct cctgttcctc ttgtgctgc taatgtgct 100

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ctgggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagt 200

gtgcactacc tctgtccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgtgctgc ctgtcatcat tgactgctgg attgacaata 300

tcaggctggt ttacaacaaa acatccagg ccaccagtt tcctgatggt 350

gtggatgtac gtgtccctgg ctttgggaag accttctcac tggagttcct 400

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gccttggtgg ctggggctac acacggggtg aggatgtccg aggggctccc 500

tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggcct 550

ccgcgagatg atcgaggaga tgtaccagct gtatgggggc ccctggtgc 600

tggttgcca cagtatgggc aacatgtaca cgctctactt tctgcagcg 650

cagccgcagg cctggaagga caagtatc cgggccttcg tgtcactggg 700

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actaccgcaa gttcttcag gacatcggt ttgaagatgg ctggtcatg 950

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<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tcttgcattt atggtgaggg ctacagcaat 200
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45

Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60

Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75

Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90

Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val
				95					100					105

Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120

Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135

Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
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Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
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Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 164

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<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

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<211> 23

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

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			20						25					30
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
			35						40					45
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
			50						55					60
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
			65						70					75
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
			80						85					90
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu

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Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly	125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro	140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu	155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val	170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile	185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu	200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg	215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu	230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr	245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly	260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg	275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala	290	295	300
Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val	305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu	320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro	335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His	350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp	365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln			

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Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
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Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
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Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
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Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
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His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585
Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala	Asp		
	590		595		600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser	Met		
	605		610		615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp	Gln		
	620		625		630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg	Leu		
	635		640		645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp	Val		
	650		655		660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala	Val		

665	670	675
Arg Pro Val Cys	Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly
680	685	690
Leu His Cys Trp	Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly
695	700	705
Pro Ile Ser Asn	Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro
710	715	720
Gln Asp Leu Cys	Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg
725	730	735
Met Leu Cys Ala	Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln
740	745	750
Gly Asp Ser Gly	Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg
755	760	765
Trp Phe Leu Ala	Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg
770	775	780
Pro Asn Tyr Phe	Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser
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Trp Ile Gln Gln	Val Val Thr	
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<210> 170

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

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<210> 173

<211> 50

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<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

tgcctatgca ctgaggaggc agaag 25

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

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<400> 176

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<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

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Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
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His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
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Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
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Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
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Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
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Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
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Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
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Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
350

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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acgcgctgga ggagtggagc agcaccgggc cggccctggg ggctgacagt 150
cggcaaagtt tggcccgaag aggaagtggc ctcaaaccac ggcaggtggc 200
gaccaggcca gaccaggggc gtcgctgcc tgcgggcggg ctgtaggcca 250
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agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
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 caccggaatg ccaattaact agagacctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
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 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	
1				5					10				15	
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp
				20					25					30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro
				35					40					45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu
				50					55					60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys
				65					70					75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro
				80					85					90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu
				95					100					105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly
				110					115					120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln
				125					130					135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His
				140					145					150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys
				155					160					165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro
				170					175					180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr

185	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His		
200	205	210
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp		
215	220	225
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp		
230	235	240
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro		
245	250	255
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn		
260	265	270
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val		
275	280	285
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala		
290	295	300
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys		
305	310	315
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg		
320	325	330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala		
335	340	345
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His		
350	355	360
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr		
365	370	375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly		
380	385	390
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg		
395	400	405
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly		
410	415	420
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr		
425	430	435
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu		
440	445	450
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys		
455	460	465
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu		

	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser		
	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp		
	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu		
	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly		
	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg		
	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn		
	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser		
	575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg		
	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro		
	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala		
	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro		
	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly		
	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro		
	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp		
	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu		
	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		
	710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gaaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgccctgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggg gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggtggtg actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtggg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450
 agttggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600
 ttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
1				5					10					15
Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
			20						25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
			35						40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
			50						55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
			65						70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
			80						85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
			95						100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
			110						115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
			125						130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 78, 212, 234, 487

<223> unknown base

<400> 191

gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50

ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100

ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150

catcgccctt tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200

ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250

aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300

atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350

gcctttgctt gatattatca actcactggg aacaacagta ttcattgtca 400

tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450

ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 192

cgttttgcag aacctactca ggcag 25

<210> 193

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgtc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgtgagc cgcggtgcc ggacgggacg 50

ggacgggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggcg 100

cactggcccg ggcgtgtctg ctgcctctgc tggcccagtg gtccttgcgc 150

gcgcgcccg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200

cgcgccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccctg 250

ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300

tcccccgcg ggcgcgcaa cttcttggcc atggtagaca acctgcaggg 350

ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400

agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450

ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500

cacataccgc tccaagggtt ttgacgtcac agtgaagtac acacaaggaa 550

gctggacggg ctctgttggg gaagacctcg tcaccatccc caaaggcttc 600

aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650

ctttttgcct gggattaaat ggaatggaat acttggecta gcttatgcca 700

catttgccaa gccatcaagt tctctggaga ccttcttoga ctccctggtg 750

acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagcccg 800

cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900

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aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
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gacagagccc agaagagggg gggcttcgca gcgagccctt gtgcagaaat 1400
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cacccgtctt caatctctgt tctgctccca gatgccttct agattcactg 1800
tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
1				5					10					15
Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
				20					25					30
Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45
Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60

Ala	Leu	Ala	Leu	Glu 65	Pro	Ala	Leu	Ala	Ser 70	Pro	Ala	Gly	Ala	Ala 75
Asn	Phe	Leu	Ala	Met 80	Val	Asp	Asn	Leu	Gln 85	Gly	Asp	Ser	Gly	Arg 90
Gly	Tyr	Tyr	Leu	Glu 95	Met	Leu	Ile	Gly	Thr 100	Pro	Pro	Gln	Lys	Leu 105
Gln	Ile	Leu	Val	Asp 110	Thr	Gly	Ser	Ser	Asn 115	Phe	Ala	Val	Ala	Gly 120
Thr	Pro	His	Ser	Tyr 125	Ile	Asp	Thr	Tyr	Phe 130	Asp	Thr	Glu	Arg	Ser 135
Ser	Thr	Tyr	Arg	Ser 140	Lys	Gly	Phe	Asp	Val 145	Thr	Val	Lys	Tyr	Thr 150
Gln	Gly	Ser	Trp	Thr 155	Gly	Phe	Val	Gly	Glu 160	Asp	Leu	Val	Thr	Ile 165
Pro	Lys	Gly	Phe	Asn 170	Thr	Ser	Phe	Leu	Val 175	Asn	Ile	Ala	Thr	Ile 180
Phe	Glu	Ser	Glu	Asn 185	Phe	Phe	Leu	Pro	Gly 190	Ile	Lys	Trp	Asn	Gly 195
Ile	Leu	Gly	Leu	Ala 200	Tyr	Ala	Thr	Leu	Ala 205	Lys	Pro	Ser	Ser	Ser 210
Leu	Glu	Thr	Phe	Phe 215	Asp	Ser	Leu	Val	Thr 220	Gln	Ala	Asn	Ile	Pro 225
Asn	Val	Phe	Ser	Met 230	Gln	Met	Cys	Gly	Ala 235	Gly	Leu	Pro	Val	Ala 240
Gly	Ser	Gly	Thr	Asn 245	Gly	Gly	Ser	Leu	Val 250	Leu	Gly	Gly	Ile	Glu 255
Pro	Ser	Leu	Tyr	Lys 260	Gly	Asp	Ile	Trp	Tyr 265	Thr	Pro	Ile	Lys	Glu 270
Glu	Trp	Tyr	Tyr	Gln 275	Ile	Glu	Ile	Leu	Lys 280	Leu	Glu	Ile	Gly	Gly 285
Gln	Ser	Leu	Asn	Leu 290	Asp	Cys	Arg	Glu	Tyr 295	Asn	Ala	Asp	Lys	Ala 300
Ile	Val	Asp	Ser	Gly 305	Thr	Thr	Leu	Leu	Arg 310	Leu	Pro	Gln	Lys	Val 315
Phe	Asp	Ala	Val	Val 320	Glu	Ala	Val	Ala	Arg 325	Ala	Ser	Leu	Ile	Pro 330
Glu	Phe	Ser	Asp	Gly 335	Phe	Trp	Thr	Gly	Ser 340	Gln	Leu	Ala	Cys	Trp 345

Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	
				395					400					405	
Val	Ile	Gly	Ala	Thr	Val	Met	Glu	Gly	Phe	Tyr	Val	Ile	Phe	Asp	
				410					415					420	
Arg	Ala	Gln	Lys	Arg	Val	Gly	Phe	Ala	Ala	Ser	Pro	Cys	Ala	Glu	
				425					430					435	
Ile	Ala	Gly	Ala	Ala	Val	Ser	Glu	Ile	Ser	Gly	Pro	Phe	Ser	Thr	
				440					445					450	
Glu	Asp	Val	Ala	Ser	Asn	Cys	Val	Pro	Ala	Gln	Ser	Leu	Ser	Glu	
				455					460					465	
Pro	Ile	Leu	Trp	Ile	Val	Ser	Tyr	Ala	Leu	Met	Ser	Val	Cys	Gly	
				470					475					480	
Ala	Ile	Leu	Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Leu	Pro	Phe	Arg	
				485					490					495	
Cys	Gln	Arg	Arg	Pro	Arg	Asp	Pro	Glu	Val	Val	Asn	Asp	Glu	Ser	
				500					505					510	
Ser	Leu	Val	Arg	His	Arg	Trp	Lys								
				515											

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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ggatgtagcc agcaactgtg 20

<210> 200
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggtc gttctcttc 19

<210> 201
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 201
gttcctgtgc ctggatgg 18

<210> 202
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

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gggcgggagc cgggagggcg gcccggcgat gaggcgctgc tgctgggcgc 150
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
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taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp	Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	80	85	90
Phe Met Ala Leu Asp	Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	100	105
Ala Thr Ala Phe	Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	115	120
His Asn Ala Gly Ile	Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	130	135
Asn Leu Leu Leu Arg	Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	145	150
His Leu Leu Leu Pro	Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	160	165
Val Val Val Ala Ser	Ala Ala His Cys Arg Gly Arg Leu Asp Phe	170	175	180
Lys Arg Leu Asp Arg	Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	190	195
Ala Tyr Ala Asp Thr	Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	205	210
Leu Ala Asn Gln Leu	Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	220	225
His Pro Gly Pro Val	Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	235	240
Gly Trp Leu Arg Pro	Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	250	255
Arg Ala Pro Arg Gly	Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	265	270
Gln Glu Gly Ile Glu	Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	280	285
His Val Glu Glu Val	Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	295	300
His Arg Leu Trp Glu	Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro	305	310	315
Gly Glu Asp Ala Glu	Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	325	330
Glu Ala Pro Ser Ser	Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	340	345
Val Ser Gln Pro Tyr	Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcattggcc ttggacttgg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150

caagcctcag gccagccacc tcccaccatc cgttggttgc tgaatgggca 200

gccctgagc atggtgcccc cagaccacac ccacctcctg cctgatggga 250

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<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
				20					25					30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60
Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu	530	535	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp	545	550	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser	560	565	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu	575	580	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp	590	595	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu	605	610	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln	620	625	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu	635	640	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser	650	655	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala	665	670	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg	680	685	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr	695	700	705

Gln Ser Gln Gln Thr	Gln Pro Pro Val	Ala Pro Gln Ala Pro	Ser
710		715	720
Ser Ile Leu Leu Pro	Ala Ala Pro Ile	Pro Ile Leu Ser Pro	Cys
725		730	735
Ser Pro Pro Ser Pro	Gln Ala Ser Ser	Leu Ser Gly Pro Ser	Pro
740		745	750
Ala Ser Ser Arg Leu	Ser Ser Ser Ser	Leu Ser Ser Leu Gly	Glu
755		760	765
Asp Gln Asp Ser Val	Leu Thr Pro Glu	Glu Val Ala Leu Cys	Leu
770		775	780
Glu Leu Ser Glu Gly	Glu Glu Thr Pro	Arg Asn Ser Val Ser	Pro
785		790	795
Met Pro Arg Ala Pro	Ser Pro Pro Thr	Thr Tyr Gly Tyr Ile	Ser
800		805	810
Val Pro Thr Ala Ser	Glu Phe Thr Asp	Met Gly Arg Thr Gly	Gly
815		820	825
Gly Val Gly Pro Lys	Gly Gly Val Leu	Leu Cys Pro Pro Arg	Pro
830		835	840
Cys Leu Thr Pro Thr	Pro Ser Glu Gly	Ser Leu Ala Asn Gly	Trp
845		850	855
Gly Ser Ala Ser Glu	Asp Asn Ala Ala	Ser Ala Arg Ala Ser	Leu
860		865	870
Val Ser Ser Ser Asp	Gly Ser Phe Leu	Ala Asp Ala His Phe	Ala
875		880	885
Arg Ala Leu Ala Val	Ala Val Asp Ser	Phe Gly Phe Gly Leu	Glu
890		895	900
Pro Arg Glu Ala Asp	Cys Val Phe Ile	Asp Ala Ser Ser Pro	Pro
905		910	915
Ser Pro Arg Asp Glu	Ile Phe Leu Thr	Pro Asn Leu Ser Leu	Pro
920		925	930
Leu Trp Glu Trp Arg	Pro Asp Trp Leu	Glu Asp Met Glu Val	Ser
935		940	945
His Thr Gln Arg Leu	Gly Arg Gly Met	Pro Pro Trp Pro Pro	Asp
950		955	960
Ser Gln Ile Ser Ser	Gln Arg Ser Gln	Leu His Cys Arg Met	Pro
965		970	975
Lys Ala Gly Ala Ser	Pro Val Asp Tyr	Ser	
980		985	

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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gaagggacct acatgtgtgt ggcc 24

<210> 213
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<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactacac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
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ttgcctgctg ctcccagggt atgaagccct ggagggccca gaggaatca 100

gcggggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgaggggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

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cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400
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 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20					25				30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40				45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met					
				65					70					75					
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu					
				80					85					90					
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr					
				95					100					105					
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile					
				110					115					120					
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser					
				125					130					135					
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala					
				140					145					150					
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu					
				155					160					165					
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu					
				170					175					180					
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr					
				185					190					195					
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro					
				200					205					210					
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala					
				215					220					225					
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg					
				230					235					240					
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu					
				245					250					255					
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His					
				260					265					270					
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln					
				275					280					285					
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys					
				290					295					300					
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro					
				305					310					315					
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val					
				320					325					330					

Ser Ala

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggt gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
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ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtgga 100
cagtgtagaaa gaaccagtgg tctcgctctg ttgccagggc tagagtgtac 150
tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctcttctgt gaggtagcca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtgg tccacctctg 350
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gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450
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 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
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 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
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 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15
Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30
His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe				
				140					145					

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tggtggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta cctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
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cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200
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gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
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ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 227
 gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgtttaaat tatcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

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gctccgagga ggtccccgga gggccctggg gacgttgggt gcaactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200
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gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
275 280 285

Ile Cys Glu Lys Arg His Asn Cys
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgatcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aagggtcgctg ggcagggcga 50
gttgggaaag cggcagcccc cgccgcccc gcagccctt ctctccttt 100
ctccacgtc ctatctgcct ctogctggag gccaggcgt gcagcatcga 150
agacaggagg aactggagcc tcattggccg gccggggcg ccggcctcgg 200
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250
cgctcccgt gtcctgccg ggtgatggaa aaccccagcc cggccgccgc 300
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggccgcccg 350
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400
tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450
gtacccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccc 500
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550
gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600
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cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700
cagcgcaggc actcgttgt ctcgtttggt gtgcgcateg tgcccagccc 750
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ggtgaccgag ataacgtcct cctctcccag ccaccggcc aactccttct 950
actaccgcg gctgaaggcc ctgcctcca tcgccagggt gacactgctg 1000
cggtgcgac agagccccag ggccttcac cctccgccc cagtctgcc 1050
cagcagggac aatgagattg tagacagcg ctcagttcca gaaacgccgc 1100
tggactgca ggtctccctg tggctgtect ggggactgtg cggaggccac 1150
tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc gggtcagcc 1200
cgccaacaac gggagccct gccccgagct cgaagaagag gctgagtgcg 1250
tcctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggcccc 1300
cggagccatg ggggtgcgg ggctcctgtg caggctcatg ctgcaggcgg 1350
ccgagggcac agggggttcc gcgctgctcc tgaccgggt gaggccgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
 aaacagcctc ctcccttccc aaccttgctt cttaggggcc cccgtgtccc 1500
 gtctgctctc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600
 tgtccttcat cgtccagggg cctgggtccc acgtggttgc agatacctca 1650
 gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcgcatcca 1700
 agcgggggcc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys	1	5	10	15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly	20	25	30	
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile	35	40	45	
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr	50	55	60	
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala	65	70	75	
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val	80	85	90	
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala	95	100	105	
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val	110	115	120	
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln	125	130	135	
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser	140	145	150	
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val	155	160	165	

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala		
	170	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe		
	185	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val		
	200	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe		
	215	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr		
	230	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala		
	245	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser		
	260	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser		
	275	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser		
	290	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro		
	305	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys		
	320	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagcccccttc tcttcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagcccccttc tcttcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgctcc gtgagggggt cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcattccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtgggtc aaagaagctc ctaaagcttg 300
cagaaatddd atccaacttt gtttggaagc ttattatgac aataccattd 350
ttcatagagt tgtgcctggt ttcatagctc aaggcggaga tctactggc 400
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaatg 500
ctggttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaaggtda caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
gaccacataa tccacacaaa ataaaaagct gtgagggtttt gtttaatcct 700
tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaaacc 750
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aattttagtt 800
tactttcatt tggagaggaa gctgagggaag aagaggagga agtaaataca 850
gttagtcaga gcatgaaggc caaaagcaaa agtagtcatg acttgcttaa 900
ggatgatcca catctcagtt ctgttccagt ttagaaaagt gaaaaagggtg 950
atgcaccaga ttagttgat gatggagaag atgaaagtgc agagcatgat 1000
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050
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aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
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tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gccctccag 1250
atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300

aggaagcaac agtcaaagaa gggaacttcc cggaagatc agacccttgc 1350
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 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
 tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500
 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
 ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600
 agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650
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 gaaaagaagt atttttgaac ctggtgtctg gttttgaaaa acaattatct 1750
 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
 catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 245
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
 1 5 10 15
 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
 20 25 30
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
 35 40 45
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
 50 55 60
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
 65 70 75
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
 80 85 90
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
 95 100 105
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
 110 115 120
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
 125 130 135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctgggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgccggtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50
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catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200
gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250
cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300
actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350
acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400
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atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500

cagacctcct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550
cctggaaagg aatcagagat gctaccacct acccgctgg atggagtctc 600
gctctgtcgc caggctggag tgcagtggca cgatctcggc tctactgcaac 650
ctccgcctcc cgggttcaag cgagtctcct gcctcagcct ctgagtgtct 700
ggggctacag gtgcctgcag gagtccctggg gccagctggc ctcgatgtac 750
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cagtgatggc ctggttcccg ggaggcgct tcctcgtggg cgctgcttct 900
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tctgcagcac aggctcggca tcttcggctt cctgagcacg gacgacagcc 1000
acgcgcgcgg gaactggggg ctgctggacc agatggcggc tctgcgctgg 1050
gtgcaggaga acatcgcagc cttcggggga gaccaggaa atgtgaccct 1100
gttcggccag tcggcggggg ccatgagcat ctcaggactg atgatgtcac 1150
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tgcccacctg gctggatgca accacaacag cacacagatc ctggtaaact 1300
gcctgagggc actatcaggg accaaggtga tgcgtgtgtc caacaagatg 1350
agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400
catgagccct gtggtggatg gtgtggtgat ccagatgac cctttggtgc 1450
tctgaccca ggggaaggtt tcctctgtgc cctaccttct aggtgtcaac 1500
aacctggaat tcaattggct cttgccttat aatatacca aggagcaggt 1550
accacttgtg gtggaggagt acctggacaa tgtcaatgag catgactgga 1600
agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650
tatgccacac tgcagactgc tctactaccac cgagaaaccc caatgatggg 1700
aatctgccct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750
ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800
tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850
taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900

caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950
 ccaccccagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000
 tagagctttt gcctgttgtg tgggacctgc actgcccttt ccagcctgac 2050
 atcccatgat gcccctctac ttactgttg acatccagtt aggccaggcc 2100
 ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150
 ttttcccttc ttcaaactct cccacccttc aatgtctcct tgtgactcct 2200
 tcttatggga ggtcgacca gactgccact gccctgtca ctgcaccag 2250
 cttggcattt accatccatc ctgctcaacc ttgttctgt ctgttcacat 2300
 tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttggtagt 2350
 ttgggatctt ctctcccacc cacacttata tccccaggg ccaactccaaa 2400
 gtctatacac aggggtggtc tcttcaataa agaagtgtg attagaaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
 1 5 10 15
 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
 20 25 30
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	
				140					145					150	
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	
				155					160					165	
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	
				170					175					180	
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	
				185					190					195	
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	
				200					205					210	
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
				215					220					225	
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	
				230					235					240	
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	
				245					250					255	
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	
				260					265					270	
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	
				275					280					285	
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	
				290					295					300	
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	
				305					310					315	
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	
				320					325					330	
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	
				335					340					345	
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	
				350					355					360	
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	
				365					370					375	
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	
				380					385					390	
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	
				395					400					405	
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	
				410					415					420	

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

agggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacggtaga agtggctgag cttcagcag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100

ggagattctg gatacagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatgget actggttcaa agcagtgact gagacaacca 250

agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350

cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400

gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450

tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500

caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgac 550

agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttggtatc 600

agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650

tgtcccatc ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700

ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750

gtcctctcct cgteccatcc ctggggccct agacccttg ggctggagct 800

gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850

acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900

ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtccctgga 950

aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000

gcctggtctg tgteacacac agcagcccc cagccaggct gagctggacc 1050

cagaggggac aggttctgag cccctcccag ccctcagacc ccggggctcct 1100

ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150

ctcggcacc actgggtccc cagcacgtct ctctcagcct ctccgtgcac 1200

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<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259
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 1 5 10 15
 Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met
 20 25 30
 Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp
 50 55 60
 Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr
 65 70 75
 Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe
 80 85 90
 Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile
 95 100 105
 Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val
 110 115 120
 Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe
 125 130 135
 Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
 140 145 150
 His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
 155 160 165
 Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
 170 175 180
 Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu
 185 190 195
 Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys
 200 205 210
 Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro
 215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgccca cccattcaaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250
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acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
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tcggatatca atgacaatga accaaaattc ctagatgaac cttatgagge 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
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aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggttaatt 1500
cagactatca gtgcagtga tagagatgaa tccatagaag agcaccattt 1550
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 ctttccatgg gattcaagac agaagttatc attgctatc tcatttgcat 1850
 tatgatcata ttgggttta ttttttgac ttgggttta aaacaacgga 1900
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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys	20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	275	280	285	

Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln		350	355	360
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr		365	370	375
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly		380	385	390
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg		395	400	405
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly		410	415	420
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp		425	430	435
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln		440	445	450
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp		455	460	465
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu		470	475	480
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp		485	490	495
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser		500	505	510
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln		515	520	525
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu		530	535	540
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn		545	550	555
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val		560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	
				575					580					585	
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	
				590					595					600	
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	
				605					610					615	
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	
				620					625					630	
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	
				635					640					645	
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
				650					655					660	
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
				665					670					675	
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
				740					745					750	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
				755					760					765	
Ser	Ala	Val	Gln	Ser	Asn	Asn									
				770											

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcttgagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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ccgccttaa cttcctccgc ggggccacgc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ccttctgcac ctgccacccc tgagccagcg 200
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250
cattctcgcc ttcttgggat ggateggcgc catcgtcagc actgccctgc 300
cccagtgag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350
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gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450
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gttcaagaat tctatgacc tatgaccca gtcaatgcca ggtacgaatt 700
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acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
gttaaaatac tcagtgttaa acatggctta atcttatttt atcttcttctc 1050
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gtaatcatac tcaaatgggg gaaggggtgc tcttaaata tatatagata 1150
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cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
				200					205					210					

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
tgatgggtggg tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
ttttagtgtc cacagcatgg tatggcaata gaancnttca acantttctat 450
gacctatga cccagtc aa tgccaggtag gaatttggtc aggctctctt 500
cactgggtgg gctgctgctt ctctctgcct tctgggaggt gccctaactt 550
gctgttcttg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cggccaggcc ntgtacgagg ggctgtggat gtcttgctg 200
tcgcagagca cggggcagat ccagtgc aaa gtctttgact ccttgctga 250
atctgagcag cacattgcaa gcaaccctg ccttgatggg ggttggcatc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcga tatttcttct tgcaggtctg gctattttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatentca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatentgac ccccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg caganacccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtggttg 250
gcatectcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450
cccagtcaat gccaggtagc aatttggcca ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctcccct cctggatgga tognccacc gtcacattgc cttccccan 50
tgaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgac cttgatgggg ttggcctcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350
caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400
cnnnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450

tcaggtctctc ttcactggct gggtgctgc ttctctctgc cttctgggag 500
gtgccctact ttgctgttcc tgtccc 526

<210> 275
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
<223> unknown base

<400> 275
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gcagcacatt ncaagcaacc ccttgccctg aaggtggttg ncatcccccc 100
tgaggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200
gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300
tgccaggtac gaatttggtc aggtctctct cactggctgg gctgctgctt 350
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<210> 276
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
<223> unknown base

<400> 276
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cagagcaccg ggcagatcca gtgcaaagtn ttgactcct tgctgaattt 150
gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcattcttc 200
tgaggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
tgcttggaa acgatgaggt gcagaagatg aggatggctg tcattggggg 300
cgcgatattt cttnttgcag gtctggctat tttagttgcc acagcatggt 350
atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccttantttg ctgttctctg gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

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cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttggtc aggetctntt cactggnttg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacnctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtga 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaaccntg 200

ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtga tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgaga tatttcttct tgcaggctctg 350

gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgcttctctc tgccttctgg gaggtgccct 500

actttgctgt tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcatctcgc ttcttgggat ggaatcggcg 50
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acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttctgtg 200
aatctgagca gcacattgca agcaaccntg ccttgatggt ggttggcatc 250
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ggggcgcgat atttcttctt gcaggtcttg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttctgttt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283
<211> 2285
<212> DNA
<213> Homo sapiens

<400> 283
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tagaggaccc ccgcccgtgc cccgaccggt ccccgccctt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200
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gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
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aagattgcct tgtagaggta gcatgcacag gatggtaa at tggtattggg 1000
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

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agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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Lys Leu Gly Asn Pro	Thr Asp Arg Asn	Val Cys Phe Lys Val	Lys
35		40	45
Thr Thr Ala Pro Arg	Arg Tyr Cys Val	Arg Pro Asn Ser Gly	Ile
50		55	60
Ile Asp Ala Gly Ala	Ser Ile Asn Val	Ser Val Met Leu Gln	Pro
65		70	75
Phe Asp Tyr Asp Pro	Asn Glu Lys Ser	Lys His Lys Phe Met	Val
80		85	90
Gln Ser Met Phe Ala	Pro Thr Asp Thr	Ser Asp Met Glu Ala	Val
95		100	105
Trp Lys Glu Ala Lys	Pro Glu Asp Leu	Met Asp Ser Lys Leu	Arg
110		115	120
Cys Val Phe Glu Leu	Pro Ala Glu Asn	Asp Lys Pro His Asp	Val
125		130	135
Glu Ile Asn Lys Ile	Ile Ser Thr Thr	Ala Ser Lys Thr Glu	Thr
140		145	150
Pro Ile Val Ser Lys	Ser Leu Ser Ser	Ser Leu Asp Asp Thr	Glu
155		160	165
Val Lys Lys Val Met	Glu Glu Cys Lys	Arg Leu Gln Gly Glu	Val
170		175	180
Gln Arg Leu Arg Glu	Glu Asn Lys Gln	Phe Lys Glu Glu Asp	Gly
185		190	195
Leu Arg Met Arg Lys	Thr Val Gln Ser	Asn Ser Pro Ile Ser	Ala
200		205	210
Leu Ala Pro Thr Gly	Lys Glu Glu Gly	Leu Ser Thr Arg Leu	Leu
215		220	225
Ala Leu Val Val Leu	Phe Phe Ile Val	Gly Val Ile Ile Gly	Lys
230		235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200
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agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

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gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
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<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
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catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
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gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgtt tgttcantta 200
aagggaccaa gctaaatttg tattggttca ttagtggaag tcaaactgtt 250
attcagagat gtttaatgca tatttaantt atttaatgta ttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttgggtg aactggtatt gctgctggag ggctgtgggc tctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
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tactcgatcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
gaaataaatg gcagtgccttt gttcacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
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gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

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gaaacctn gn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctotta aaatgacacc 150
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
cccaggetgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcatat tt aanttattta atgtatttca tntcatgttt tcttattgtc 550
acaagggtac agttaatgct gcgtgctgct gaantctgtt ggggtgaantg 600
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<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
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<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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ggctggctga gaggctccca gctgcagcgt ccccgcccgc ctccctcgga 100
gctctgatct cagctgacag tgcctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagtcca gtgccatgat catggtttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
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attttccacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350
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ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550
cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600
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cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750
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 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20										25					30				
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu					
				35					40					45					
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr					
				50					55					60					
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu					
				65					70					75					
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn					
				80					85					90					
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu					
				95					100					105					
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg					
				110					115					120					
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp					
				125					130					135					
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu					
				140					145					150					
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu					
				155					160					165					
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly					
				170					175					180					
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser					
				185					190					195					
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala					
				200					205					210					
Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu					
				215					220					225					
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln					
				230					235					240					
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys					
				245					250					255					
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp					
				260					265					270					
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala					
				275					280					285					
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys					
				290					295					300					
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp					

	305		310		315
Arg Ala Asp Gln	Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp	Glu		
	320		325		330
Ser Asn Asp Leu	Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly	Ser		
	335		340		345
Thr Gly Ser Gly	Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys	Lys		
	350		355		360
Asn Trp Lys Arg	Lys Ile Ile Ala Val	Tyr Ser Gly His Gln	Trp		
	365		370		375
Val Asp Val His	Gly Val Gln Lys Asp	Tyr Asn Val Ala Val	Arg		
	380		385		390
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His	Gly		
	395		400		405
Asn Asp Ala Asn	Cys Ala Tyr Gly				
	410				

<210> 297
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 297
 gcacatctgcag gagagagcga aggg 24

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
 catcggttccc gtgaatccag aggc 24

<210> 299
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
 gaagggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300

<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300

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<210> 301
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 301

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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe	
				425					430					435	
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val	
				440					445					450	
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp	
				455					460					465	
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro	
				470					475					480	
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro	
				485					490					495	
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln	
				500					505					510	
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser	
				515					520					525	

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

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 ctgggcgggg cgctgtggct ggcggcccgc cgttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccgg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaaac agcggcctgg gccgcgccac ggccgcccag 250
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 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
 agtgatgggt ggccctgctaa aataggaaca aggagtataa gagctgttta 1100
 taaaactgca tatcagttat atctgtgatc aggaatgggtg tggattgaga 1150
 acttggtact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtattttgg agttactgaa aaattatitt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatatit gtcagaatta agtgactcaa agtgctatcg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttgggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
 cacaagtctt acttgggaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5					10				15	
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20						25				30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
			35						40				45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
			50						55				60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
			65						70				75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
			80						85				90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly

	95	100	105
Val Gly Glu Leu	Ile Val Arg Glu Leu	Asp Leu Ala Ser Leu	Arg
	110	115	120
Ser Val Arg Ala	Phe Cys Gln Glu Met	Leu Gln Glu Glu Pro	Arg
	125	130	135
Leu Asp Val Leu	Ile Asn Asn Ala Gly	Ile Phe Gln Cys Pro	Tyr
	140	145	150
Met Lys Thr Glu	Asp Gly Phe Glu Met	Gln Phe Gly Val Asn	His
	155	160	165
Leu Gly His Phe	Leu Leu Thr Asn Leu	Leu Leu Gly Leu Leu	Lys
	170	175	180
Ser Ser Ala Pro	Ser Arg Ile Val Val	Val Ser Ser Lys Leu	Tyr
	185	190	195
Lys Tyr Gly Asp	Ile Asn Phe Asp Asp	Leu Asn Ser Glu Gln	Ser
	200	205	210
Tyr Asn Lys Ser	Phe Cys Tyr Ser Arg	Ser Lys Leu Ala Asn	Ile
	215	220	225
Leu Phe Thr Arg	Glu Leu Ala Arg Arg	Leu Glu Gly Thr Asn	Val
	230	235	240
Thr Val Asn Val	Leu His Pro Gly Ile	Val Arg Thr Asn Leu	Gly
	245	250	255
Arg His Ile His	Ile Pro Leu Leu Val	Lys Pro Leu Phe Asn	Leu
	260	265	270
Val Ser Trp Ala	Phe Phe Lys Thr Pro	Val Glu Gly Ala Gln	Thr
	275	280	285
Ser Ile Tyr Leu	Ala Ser Ser Pro Glu	Val Glu Gly Val Ser	Gly
	290	295	300
Arg Tyr Phe Gly	Asp Cys Lys Glu Glu	Glu Leu Leu Pro Lys	Ala
	305	310	315
Met Asp Glu Ser	Val Ala Arg Lys Leu	Trp Asp Ile Ser Glu	Val
	320	325	330
Met Val Gly Leu	Leu Lys		
	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229
<223> unknown base

<400> 304
ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
gcaagaaaat tntgggatat cagtgaagtg atgggtngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaattat ctgcctggct t 521

<210> 305
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 305
ccaggaaatg ctccaggaag agcc 24

<210> 306
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 306
gcccatgaca ccaaattgaa gagtgg 26

<210> 307
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccttttcta acccaaccca acctagccca gtcccagccg 100
ccagcgctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150
cttcctatcc ttaccgacc tcagatgctc ccttctgctc ctggtaactt 200
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300
tgactgggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttctcttctg ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
gctttaaaaaa cttgaaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
tttatTTTga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195	

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 48
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tgcgcgcngg agcccggtc 50
gagaggacna ggtgccgtg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagegectg tcctgtenc ggancccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccgcacc tcagatgctc ccttctgctc ctggtaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttcccta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggcccttctgc tacatgctgg 50

cgtctgtgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaaata tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggtat ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttcacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatgggtat tacgtataaa ttaatatataa atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttggc ttcatgtgaa cagtatctaa ttataaatta 850
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950
 atacattttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatatact tgctttaatt ctttaagcata agtaaacaatg atataaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10					15
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25					30
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40					45
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55					60
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70					75
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85					90
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100					105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatcccct tgtactcca gagtacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgccctt cttggcatat catatttga ggtatatgag tagaccagt 200
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgatc agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tggcgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgetgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggcctgaagca ttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagagggtg caggctgttt 300
tcaatttgct agtttggtga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500
 aactctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
 gttatatcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgct ctctcgggtga tggatttgc ttggatttgc tgtgcaactg 850
 ttgctacagc tgtggagcag tatgttccct ctgagaagct gaggatctat 900
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
 caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10					15
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100					105

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatcga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctggtag gtcattctgg agtgacatga tggactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

cacactggcc ggatctttta ggtcccttg accttgacca agggctcngga 50
aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100
cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggccttgcc ggaggttcgg ggaccgcttc ggctgaagca 200
ttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagaggttg caggtgttt tcaatttgc agtttgtgga tgatggaatt 350
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgcaaaa 500
atgcacctac tcttctctt aactctggtg aggtcattct ggagtacat 550
gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggagggttc ggggaccgct tcggtgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgccccggag gtggggcgcc gctggggccg gccgcacgg gcttcactctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccg cggtgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggcttc tggtaaggg 850
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950
 tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttg 1350
 ttgttttaaa tgcgtctgtt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaactttt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgttgt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
1				5					10				15	

Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25					30	

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp	35	40	45
Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg	50	55	60
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg	65	70	75
Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln	95	100	105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr	110	115	120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu	125	130	135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys	140	145	150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe	155	160	165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp	170	175	180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp	185	190	195
Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys	200	205	210
Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln	215	220	225
Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu	230	235	240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His	245	250	255
Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu	260	265	270
Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln	275	280	285
Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg	290	295	300
Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu	305	310	315

Ser Lys Val Leu	Pro Phe Phe Glu Arg	Pro Asp Phe Gln Leu Phe
320	325	330
Thr Gly Asn Lys	Ile Gln Asp Glu Glu	Asn Lys Met Leu Leu Leu
335	340	345
Glu Ile Leu His	Glu Ile Lys Ser Phe	Pro Leu His Phe Asp Glu
350	355	360
Asn Ser Phe Phe	Ala Gly Asp Lys Lys	Glu Ala His Lys Leu Lys
365	370	375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp
380	385	390
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr
395	400	405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu
410	415	420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu
425	430	435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile
440	445	450
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln
455	460	465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50

ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100

nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150

ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200

caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250

attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300

tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtggtacca ttctngagc gccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcac ttctttgca tttgatgag aattcatttt 500
tttgctg 507

<210> 339

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

aagctgccgg agctgcaatg 20

<210> 340

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 340

ttgcttctta atcctgagcg c 21

<210> 341

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

aaaggaggac tttcgactgc 20

<210> 342

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

agagattcat ccactgctcc aagtcg 26

<210> 343

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta ctgggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggccgacgcg tgggcggacg cgtgggttg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgtcct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttggtat acagtgtctt acaacatgtt ggggggtggac agcgatggat 300
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg gggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agagggtggt ggcagtgtct ctgaagggtc ataaaagaaa 550
aaagagaagt gtggaaggg aaaatggtct gtgtggagg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgcccggt tggatgcttc 800
attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc taccctcatt 950
gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaatata aaaattagct 1150
gggtgcgcta gtgcatgcct gtaatctcat ctactcgga ggctaagaca 1200
ggagactctc acttcaaccc aggaggtgga gggtgcggtg agccaagatt 1250
gtgcctctgc actctagcgt ggggtgacaga gtaagcgaga ctccatctca 1300
aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
1				5					10					15
Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
cacagtcccc caccatcact cntcccatc cttccaactt tattttttagc 50
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagaggggac agaggccaga ggactttctca tactggacag aaaccgatca 150
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttctt 200
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300
gggggtggac agcgatggat gctgggtggg gccccctggg atgggccttc 350
agggcagccgg aggggggacg tttatcgctg ccctgtaggg gggggcccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaaactcccc ttctgtcactc acctgttctt gcccttgggtg ttctt 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttctctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaa atggctgaga tggacagaat 200
gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagt atcgcgctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
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atgacatcac ggccactgtg ccatacaacc ttctgtgctag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttaccgcac ctgggatgga gatcaccaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagacc tggtgccgag gaacatgtca aaatgggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
actgtgtgaa ggcccagaca ttctgtaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt ggagggtgcaa ggagaggcca ttcccctggt 950
actggccctg ttgacctttg ttggcttcat gctgatccct gtggctcgtgc 1000

cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
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 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
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 gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350
 gtctaacaga aactgactg aggcttaggg gatgtgacct ctagactggg 1400
 ggctgccact tgctggctga gcaacctgg gaaaagtgc ttcattccctt 1450
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 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
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 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1				5				10					15	

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
				20				25					30	

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcatctcttg atgtggagcc cagtgategc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450
tggatcccca gcagctggtg ctcaactcact gaaggctcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
agaaactcaa ccatccttac ccgaacctggg atggagatca ccaaagatgg 650
cttncaacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgtgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgaggagc aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
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agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
				20					25					30
Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45
Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
				50					55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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gcagctactg ctcagaaaacg ctggggcgcc caccctggca gactaacgaa 150
gcagctcctt tcccaccca actgcaggtc taattttgga cgctttgcct 200
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250
ctgcagtcag caccacgct gcccccggac gctcgggtgct caggcccttc 300
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aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550
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 aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950
 attttttttc tgctgggtgga tttacatatt aaattttttc tgctgggtgga 3000
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu		35	40	45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn		50	55	60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln		65	70	75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val		80	85	90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp		95	100	105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu		110	115	120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln		125	130	135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His		140	145	150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys		155	160	165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly		170	175	180
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile		185	190	195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly		200	205	210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser		215	220	225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys		230	235	240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu		245	250	255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His		260	265	270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser		275	280	285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg		290	295	300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala		305	310	315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
gcgagagacaa ggcagagcg cagcgacgg ccacagacag ccctgggcat 50
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ggccagcgcc ctcccatgt cctgctccc acgcgcgcc cctccggtea 200
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accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccggc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccagggtac 400
 cgaggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450
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 ataaaatata tttgaaatgt aaaaaaaaaa aaaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20				25					30

Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45

Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60

Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75

Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90

Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95				100						105

Arg	Arg	Val	Tyr	Glu	Glu
				110	

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150
caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200
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<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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			20						25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
			35						40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
			50						55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
			65						70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
			80						85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
			95						100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
			110						115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
			125						130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
			140						145					150

Ser Asn Asp Arg	Gly Glu Asp Glu Asp	Ile His Asp Gln Asn Ser
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Lys Lys Pro Val	Met Val Tyr Ile His	Gly Gly Ser Tyr Met Glu
170	175	180
Gly Thr Gly Asn	Met Ile Asp Gly Ser	Ile Leu Ala Ser Tyr Gly
185	190	195
Asn Val Ile Val	Ile Thr Ile Asn Tyr	Arg Leu Gly Ile Leu Gly
200	205	210
Phe Leu Ser Thr	Gly Asp Gln Ala Ala	Lys Gly Asn Tyr Gly Leu
215	220	225
Leu Asp Gln Ile	Gln Ala Leu Arg Trp	Ile Glu Glu Asn Val Gly
230	235	240
Ala Phe Gly Gly	Asp Pro Lys Arg Val	Thr Ile Phe Gly Ser Gly
245	250	255
Ala Gly Ala Ser	Cys Val Ser Leu Leu	Thr Leu Ser His Tyr Ser
260	265	270
Glu Gly Leu Phe	Gln Lys Ala Ile Ile	Gln Ser Gly Thr Ala Leu
275	280	285
Ser Ser Trp Ala	Val Asn Tyr Gln Pro	Ala Lys Tyr Thr Arg Ile
290	295	300
Leu Ala Asp Lys	Val Gly Cys Asn Met	Leu Asp Thr Thr Asp Met
305	310	315
Val Glu Cys Leu	Arg Asn Lys Asn Tyr	Lys Glu Leu Ile Gln Gln
320	325	330
Thr Ile Thr Pro	Ala Thr Tyr His Ile	Ala Phe Gly Pro Val Ile
335	340	345
Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln
350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly
365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly
380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp
395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr
410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu
425	430	435

Thr Arg Arg Lys	Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His	Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
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His	Ser	Thr	Thr	Arg	Val									
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<210> 376
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377
 aacccccgag ccaaaagatg gtcac 25

<210> 378
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 378
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<210> 379
 <211> 2461
 <212> DNA

<213> Homo sapiens

<400> 379

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cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtgg 200
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<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20					25					30

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly				35	40	45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro				50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met				65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp				80	85	90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe				95	100	105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln				110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr				125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys				140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu				155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn				170	175	180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr				185	190	195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp				200	205	210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met				215	220	225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val				230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser				245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys				260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu				275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro				290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe				305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 382
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 382
cactctccag gctgcatgct cagg 24

<210> 383
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<212> DNA
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<400> 383
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<210> 384
<211> 3150
<212> DNA
<213> Homo sapiens

<400> 384
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala
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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser	Cys Tyr Cys Pro Val	Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu	Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr	Tyr Gly Glu Met Ala	Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro	Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His	Asn Val Ser Phe Pro	Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu	His Phe Lys Val Ile	Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys	Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn	Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu	Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp	Val Thr Leu Ser Pro	Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe	Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro	Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr	Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His	Lys Arg Ser Pro Lys	Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp	Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala	Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386
ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

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gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccctg 200
cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250
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gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgccct 600
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 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggagggt 3250
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 aaactctatc tca 3313

<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	
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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	
				20					25					30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	
				35					40					45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	
				50					55					60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	
				65					70					75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	
				80					85					90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	
				95					100					105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	
				110					115					120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	
				125					130					135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	
				140					145					150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	
				155					160					165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	
				170					175					180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	
				185					190					195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	
				200					205					210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	
				215					220					225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	
				230					235					240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	
				245					250					255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	
				260					265					270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	
				275					280					285	

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly	Val Glu Leu Ala Pro	Arg Ser Ala Glu Pro	Gly
	575	580	585
Tyr Leu Val Thr	Lys Val Val Ala Val	Asp Arg Asp Ser Gly	Gln
	590	595	600
Asn Ala Trp Leu	Ser Tyr Arg Leu Leu	Lys Ala Ser Glu Pro	Gly
	605	610	615
Leu Phe Ser Val	Gly Leu His Thr Gly	Glu Val Arg Thr Ala	Arg
	620	625	630
Ala Leu Leu Asp	Arg Asp Ala Leu Lys	Gln Ser Leu Val Val	Ala
	635	640	645
Val Gln Asp His	Gly Gln Pro Pro Leu	Ser Ala Thr Val Thr	Leu
	650	655	660
Thr Val Ala Val	Ala Asp Ser Ile Pro	Gln Val Leu Ala Asp	Leu
	665	670	675
Gly Ser Leu Glu	Ser Pro Ala Asn Ser	Glu Thr Ser Asp Leu	Thr
	680	685	690
Leu Tyr Leu Val	Val Ala Val Ala Ala	Val Ser Cys Val Phe	Leu
	695	700	705
Ala Phe Val Ile	Leu Leu Leu Ala Leu	Arg Leu Arg Arg Trp	His
	710	715	720
Lys Ser Arg Leu	Leu Gln Ala Ser Gly	Gly Gly Leu Thr Gly	Ala
	725	730	735
Pro Ala Ser His	Phe Val Gly Val Asp	Gly Val Gln Ala Phe	Leu
	740	745	750
Gln Thr Tyr Ser	His Glu Val Ser Leu	Thr Thr Asp Ser Arg	Lys
	755	760	765
Ser His Leu Ile	Phe Pro Gln Pro Asn	Tyr Ala Asp Met Leu	Val
	770	775	780
Ser Gln Glu Ser	Phe Glu Lys Ser Glu	Pro Leu Leu Leu Ser	Gly
	785	790	795
Asp Ser Val Phe	Ser Lys Asp Ser His	Gly Leu Ile Glu Val	Ser
	800	805	810
Leu Tyr Gln Ile	Phe Phe Leu Phe Phe	Phe Asn Cys Ser Val	Ser
	815	820	825
Gln Ala Gly Val	Gln Arg Tyr Asp His	Ser Ser Leu Arg Pro	Gln
	830	835	840
Thr Pro Arg Leu	Lys Gln Leu Ser His	Leu Cys Leu Arg Cys	Asn
	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
				905					910					915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaaaccca ttcgcagcct 300
 tggcaggcgg ccttgttcca gggccagcaa ctactctgtg gcggtgtcct 350
 tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
 acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450
 caagaaatac ctgtggttca gtccatccca caccctgct acaacagcag 500
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 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900
 tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggcgg gctgagcgcc tcctgcggcc cggcctgcgc 50

gccccggccc gccgcgccgc ccacgcccc accccggccc gcgcccccta 100

gccccgccc gggcccgccg ccgcgcccgc gccaggtga gcgctccgcc 150

cgccgcgagg ccccgccccg gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatectccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgccgcc 300

gccgcctctg cctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

gggcccgggc cgggcccgtag cggcggcgcc tggatgcgga cccggccgcg 450

gggagacggg cgcccgcgcc gaaacgaatt tcagtccccg acgcgccccg 500

cccaaccct acgatgaaga gggcgccgc tggagggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccaggt 600

gcctgcgtat gctacaatga gcccaagggt acgacaagct gccccagca 650

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 cccggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000
 acaacgcgct gcaggcactg cctgatgaca ccttcgcgca cctgggcaac 1050
 ctcacacacc tcttcctgca cggcaaccgc atctccagcg tgcccagagcg 1100
 cgccttcctg gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150
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 aactctatc tgtttgcaa caatctatca gcgctgcca ctgaggccct 1250
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<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val	
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala	
			20						25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
			35						40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
			50						55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
			65						70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
			80						85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
			95						100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
			110						115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
			125						130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
			140						145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
			155						160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
			170						175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
			185						190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
			200						205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
			215						220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
			230						235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
			245						250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
			260						265					270	

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser Glu Val	
	275	280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys Arg	
	290	295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr Gly Pro	
	305	310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu Pro Leu	
	320	325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
	335	340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
	350	355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
	365	370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
	380	385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
	395	400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
	410	415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
	425	430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
	440	445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
	455	460	465
Leu Trp Thr Val	Leu Gly Pro Cys		
	470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgacga 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gaggaattc 350

tccaggcggg gggttagggt tgtttccaga gggaaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttggtgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaattgtg gtgaaagtat 600

cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650

ttagatgtag gccaaaacaa tattgagaac tatataatca gcccgaactc 700

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 attttggtggc atttccatgc caatgtttat ttccccaat ttgtgtgtat 2650
 gtaatatgt acggatttac tcttgatttt tctcatgttc tttctccctt 2700
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<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu
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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu
			20					25					30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
			35					40					45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50					55					60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65					70					75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80					85					90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95					100					105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110					115					120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125					130					135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140					145					150	

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
	440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
	455	460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
	470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
	485	490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
	500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
	515	520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
	530	535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
	545	550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
	560	565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
	575	580	585
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
	590	595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
	605	610	615
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
	620	625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
	635	640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
	650	655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
	665	670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
	680	685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
	695	700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
	710	715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tctctctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
 cggtcgacga ccgccccgcg tcatgcggt cctcggctgg tggcaagtat 150
 tgctgtgggt gctgggaactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
 ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atgggccagg 300
 acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500
 cacttccttg acagagaaga ggagtattac acagagccag aagtggcgga 550
 atctgacga gccccgacag aggactccaa taacactgaa agtctgaaat 600
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
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 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
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 caataagcaa atgcaaaaat attcaatag 1379

<211> 360

<212> PRT

<213> Homo sapiens

<400> 410

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				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu	
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys	
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro	
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu	
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu	
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu	
350	355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

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<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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Pro Asp Phe Ser Tyr	Lys Arg Ser Asn	Cys Lys Pro Ile Pro	Val
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Asn Leu Gln Leu Cys	His Gly Ile Glu	Tyr Gln Asn Met Arg	Leu
50		55	60
Pro Asn Leu Leu Gly	His Glu Thr Met	Lys Glu Val Leu Glu	Gln
65		70	75
Ala Gly Ala Trp Ile	Pro Leu Val Met	Lys Gln Cys His Pro	Asp
80		85	90
Thr Lys Lys Phe Leu	Cys Ser Leu Phe	Ala Pro Val Cys Leu	Asp
95		100	105
Asp Leu Asp Glu Thr	Ile Gln Pro Cys	His Ser Leu Cys Val	Gln
110		115	120
Val Lys Asp Arg Cys	Ala Pro Val Met	Ser Ala Phe Gly Phe	Pro
125		130	135
Trp Pro Asp Met Leu	Glu Cys Asp Arg	Phe Pro Gln Asp Asn	Asp
140		145	150
Leu Cys Ile Pro Leu	Ala Ser Ser Asp	His Leu Leu Pro Ala	Thr
155		160	165
Glu Glu Ala Pro Lys	Val Cys Glu Ala	Cys Lys Asn Lys Asn	Asp
170		175	180
Asp Asp Asn Asp Ile	Met Glu Thr Leu	Cys Lys Asn Asp Phe	Ala
185		190	195
Leu Lys Ile Lys Val	Lys Glu Ile Thr	Tyr Ile Asn Arg Asp	Thr
200		205	210
Lys Ile Ile Leu Glu	Thr Lys Ser Lys	Thr Ile Tyr Lys Leu	Asn
215		220	225
Gly Val Ser Glu Arg	Asp Leu Lys Lys	Ser Val Leu Trp Leu	Lys
230		235	240
Asp Ser Leu Gln Cys	Thr Cys Glu Glu	Met Asn Asp Ile Asn	Ala
245		250	255
Pro Tyr Leu Val Met	Gly Gln Lys Gln	Gly Gly Glu Leu Val	Ile
260		265	270
Thr Ser Val Lys Arg	Trp Gln Lys Gly	Gln Arg Glu Phe Lys	Arg
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Ile Ser Arg Ser Ile	Arg Lys Leu Gln	Cys	

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<211> 21
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
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<210> 418
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
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<210> 419
<211> 1830
<212> DNA
<213> Homo sapiens

<400> 419
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gtgttggttc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
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<210> 420
<211> 560
<212> PRT
<213> Homo sapiens

<400> 420

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				20					25					30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	
				35					40					45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	
				50					55					60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	
				65					70					75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	
				80					85					90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	
				95					100					105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	
				110					115					120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	
				125					130					135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	
				140					145					150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	
				155					160					165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	
				170					175					180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	
				185					190					195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	
				200					205					210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	
				215					220					225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	
				230					235					240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	
				245					250					255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu
260	265	270
Glu Gln Ile Leu Cys	Ala Ser Gly His	Ser Ser Gly Phe Ser Gly
275	280	285
Leu Cys Gly Ala Leu	Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu
290	295	300
Ala Leu Gly Pro Tyr	Val Asp Arg Thr	Lys His Phe Thr Glu Ala
305	310	315
Thr Lys Ile Gly Leu	Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe
320	325	330
Ala Leu Val Ser Gln	Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala
335	340	345
Thr Cys Ser Leu Leu	Gly Leu Phe Gly	Phe Ser Val Gly Pro Val
350	355	360
Ala Met Glu Leu Ala	Val Glu Cys Ser	Phe Pro Val Gly Glu Gly
365	370	375
Ala Ala Thr Gly Met	Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile
380	385	390
Leu Ile Met Leu Ala	Met Thr Ala Leu	Thr Val Arg Arg Ser Glu
395	400	405
Pro Ser Leu Ser Thr	Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp
410	415	420
Thr Val Ser Leu Leu	Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser
425	430	435
Cys Ile Leu Ala Val	Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln
440	445	450
Ala Glu Ser Gly Glu	Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly
455	460	465
Ala Asp Ser Gly Pro	Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala
470	475	480
Gly Val Leu Gly Pro	Ser Thr Ala Thr	Pro Glu Cys Thr Ala Arg
485	490	495
Gly Ala Ser Leu Glu	Asp Pro Arg Gly	Pro Gly Ser Pro His Pro
500	505	510
Ala Cys His Arg Ala	Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr
515	520	525
Asp Ala Pro Ser Arg	Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala
530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
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Pro Trp Val Ile Thr
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag cctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cgggtcaata aacctggacg ctgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

aagggtgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300

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<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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	20					25					30
Thr Val Lys Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val
	35					40					45
Ile Gly Lys Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg
	50					55					60
Gln Ala Gly Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu
	65					70					75
Pro Ile Gln Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg
	80					85					90
Arg Leu Asp Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu
	95					100					105
Val Ser Phe Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His
	110					115					120
Val Glu Ile Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe
	125					130					135
Pro Lys Gly Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu
	140					145					150
Arg Thr Arg Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly
	155					160					165
Pro Asn Thr Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe
	170					175					180
Ala Leu Asp Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu
	185					190					195
Leu Ile Val Val	Lys	Glu	Leu	Asp	Arg	Glu	Ile	His	Ser	Phe	Phe
	200					205					210
Asp Leu Val Leu	Thr	Ala	Tyr	Asp	Asn	Gly	Asn	Pro	Pro	Lys	Ser
	215					220					225
Gly Thr Ser Leu	Val	Lys	Val	Asn	Val	Leu	Asp	Ser	Asn	Asp	Asn
	230					235					240
Ser Pro Ala Phe	Ala	Glu	Ser	Ser	Leu	Ala	Leu	Glu	Ile	Gln	Glu
	245					250					255
Asp Ala Ala Pro	Gly	Thr	Leu	Leu	Ile	Lys	Leu	Thr	Ala	Thr	Asp
	260					265					270
Pro Asp Gln Gly	Pro	Asn	Gly	Glu	Val	Glu	Phe	Phe	Leu	Ser	Lys
	275					280					285
His Met Pro Pro	Glu	Val	Leu	Asp	Thr	Phe	Ser	Ile	Asp	Ala	Lys
	290					295					300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305		310 315
Pro Ala Tyr Glu Val	Asp Val Gln Ala Arg Asp Leu Gly Pro Asn	
320		325 330
Pro Ile Pro Ala His Cys Lys Val Leu	Ile Lys Val Leu Asp Val	
335		340 345
Asn Asp Asn Ile Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro	
350		355 360
Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu		
365		370 375
Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His		
380		385 390
Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr		
395		400 405
Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg		
410		415 420
Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln		
425		430 435
Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile		
440		445 450
Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr		
455		460 465
Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile		
470		475 480
Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val		
485		490 495
Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile		
500		505 510
Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr		
515		520 525
Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser		
530		535 540
Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu		
545		550 555
Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu		
560		565 570
Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr		
575		580 585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750
Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
gtaagcacat gcctccagag gtgc 24

<210> 427
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
gtgacgtgga tgcttgggat gttg 24

<210> 428
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 428
tggacacctt cagtattgat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429
<211> 2037
<212> DNA
<213> Homo sapiens

<400> 429
cggaacgcgtg ggccggacgcg tgggggagag ccgcagtcctt ggctgcagca 50
cctgggagaa ggcagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100
ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150
tgagtttcct catcgactcc agcatcatga ttacctcca gatactatct 200
tttgattttg ggtggctttt cttcatgcgc caattgttta aagactatga 250
gatacgtcag tatgtgttac aggtgatctt ctccgtgacg ttgcatttt 300

cttgacccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400
gatcctgggtt ttcattggtgc ctttttacat tggctatttt attgtgagca 450
atatccgact actgcataaa caacgactgc ttttttcctg tctcttatgg 500
ctgaccttta tgtatttctt ctggaaacta ggagatccct tccccattct 550
cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600
gtgtgattgg agtgactctc atggctcttc tttctggatt tgggtgctgc 650
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ggatattcta gccctggaac ggcgactgct gcaaaccatg gatatgatca 750
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taccacttca gcatcaggaa gtgaaaatct tactcttatt caacaggaag 900
tggatgcttt ggaagaatta agcaggcagc tttttctgga aacagctgat 950
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 gtgaaaaata cactggaact ctggggcaag acatgtctat ggtagctgag 1850
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 ttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
 aaaaaaaaaa agggcgggcg cgactctaga gtcgacctgc agaagcttgg 2000
 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

Met	Ser	Phe	Leu	Ile	Asp	Ser	Ser	Ile	Met	Ile	Thr	Ser	Gln	Ile
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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser
			125						130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
			140						145					150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
			155						160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
			170						175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
	425	430	435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
	440	445	450
Lys Gln Met Ala	Pro		
	455		

<210> 431

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

<400> 431
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togactccag catcatgatt acctcccnga nactatTTTT tggatttggg 100
tggtttttct tcnngcggaa tgtttaaaga ctatgagata cgtcagtatg 150
ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgtaa 250
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttntca 300
tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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gccaagggtt tctttnttga attccgggtt nngnatacct tcccagaaaa 100
tatttttttg atttggggta gnttttttcc atgcgccaat tgtttaaaga 150
ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200
cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
ttgaatagca gctcccgtaa tttcactgg aaaatgaacc tgtgtgtaat 300
tctgctgac ctggttttca tgggtgccttt ttacattggc tattttattg 350
tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
ttatggctga cctttatgta tttntnttgg aaantaggag atccctttcc 450

cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgttataa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

ctcgcgagc gatcgccca tggccggggc tcggagccgc gacccttggg 50

gggcctccgg gatttgctac ctttttggtt ccctgctcgt cgaactgctc 100

ttctcacggg ctgtgcctt caatctggac gtgatgggtg ccttgcgcaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccag agctggctgc tgggtgggtgc tccccaggcc 250

ctggctcttc ctgggcagca ggcgaatgc actggaggcc tcttcgcttg 300

cccgttgagc ctggaggaga ctgactgcta cagagtggac atcgaccagg 350

gagctgatat gcaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400

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 a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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				20					25					30
Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgcctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcaggagct gagtggacgg ctcgagacgg cggcgcgctgc 50
agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100
ggagctgcga gcacagtgtt ggctcacaac aagatgctca aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcgagctg 200
ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
aagcagtgcc cagtggctta tcccagccct gtttgtggtt cagatggtca 600
tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650
aacagatctc agtcaaattgt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750
caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950
 tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000
 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
 ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100
 atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150
 ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200
 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250
 gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300
 tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350
 cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400
 gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450
 acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500
 cctattttaa attatcttct tcccataaa caaaatgatt ctaaacctca 1550
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 aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagtg 1700
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 caaaatgaca gctagtgcct gggatcgta atgttaattt tttgaaagat 1800
 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp
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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20				25					30	

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

	320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly	335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp	350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn	365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe	380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu	395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu	410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr	425	430	435

Ile

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
 cagcaatatt cagaagcggc aaggg 25

<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

cagactccag atttcctgt caaccacgag gagtccagag aggaaacgcg 50

gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100

cagggatggg cgacaagatc tggtgtccct tccccgtgct ccttctggcc 150

gctctgcctc cggtgctgct gcctggggcg gccggcttca caccttcct 200

cgatagcgac ttcaccttta ccctccccc gcggcagaag gagtgcttct 250

accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300

gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350

aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400

ctgaagttag tgattacatg ttctgctttg acaatacatt cagcaccatt 450

tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500

ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550

tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600

agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650

tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700

ctatggttaa tttagtggc atggtggtgg tgtcagccat tcaagtttat 750

atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800

caaaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850

tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900

aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950

tgtgcaagta atcctgctga tccagttgta ctttaagtgtg taacaggaat 1000

attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050

tttcctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100

gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150

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aaatcttttag actacaaaag cccaactttt ctctattttac atatgcatct 1300
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cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400
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 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val	Leu Asp Gly Ala Gly	Leu Asp Ile Asp Phe His
65	70	75
Leu Ala Ser Pro	Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	
80	85	90
Ser Asp Gly Val	His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	
95	100	105
Phe Cys Phe Asp	Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	
110	115	120
Phe Phe Glu Leu	Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	
125	130	135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	
140	145	150
Met Lys Leu Glu	Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	
155	160	165
Arg Leu Ser Lys	Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	
170	175	180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	
185	190	195
Asn Phe Trp Ser	Met Val Asn Leu Val Val Met Val Val Val Ser	
200	205	210
Ala Ile Gln Val	Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	
215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50
agcataccag atctcaccag agagtgcag aactatgct gcctcccatg 100
gccctgcccc gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150
tcaggttcaa ggtgaagaaa ccagaagga actgcctct ccacggatca 200
gctgtcccaa aggtctcaag gcctatggct cccctgcta tgcttggtt 250
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
ctctggaaaa ctggtgtctg tgctcagtgg ggctgagga tccttcgtgt 350
cctccctggt gaggagcatt agtaacagct actatacat ctggattggg 400
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550
ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600
gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650
gtcatcatg gacatgagac cagtgtgaag actcacctg gaagagaata 700
ttctcccaa actgcctac ctgactacct tgtcatgac ctcttcttt 750
ttctttttt ttacettca ttccaggctt ttctctgtct tccatgtctt 800
gagatctcag agaataataa taaaatggt actttataaa aaaaaaaaaa 850
aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT

<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
				20					25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
				35					40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
				50					55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
				65					70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
				80					85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
				95					100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
				110					115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
				125					130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
				140					145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
				155					160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
				170					175						

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

ccagtctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50

tgggggtgaga gcacagagga gtgggcccgg accatgcggg ggacgcggct 100

ggcgctcctg gcgctgggtgc tggctgcctg cggagagctg gcgccggccc 150

tgcgctgcta cgtctgtccg gagccacacag gagtgtcgga ctgtgtcacc 200

atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250

ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
tccgactgta gaggccccgc ccacccccat ggccttatgc ggcccagccc 500
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454

<211> 125

<212> PRT

<213> Homo sapiens

<400> 454

Met	Arg	Gly	Thr	Arg	Leu	Ala	Leu	Leu	Ala	Leu	Val	Leu	Ala	Ala
1					5				10					15
Cys	Gly	Glu	Leu	Ala	Pro	Ala	Leu	Arg	Cys	Tyr	Val	Cys	Pro	Glu
			20						25					30
Pro	Thr	Gly	Val	Ser	Asp	Cys	Val	Thr	Ile	Ala	Thr	Cys	Thr	Thr
			35						40					45
Asn	Glu	Thr	Met	Cys	Lys	Thr	Thr	Leu	Tyr	Ser	Arg	Glu	Ile	Val
			50						55					60
Tyr	Pro	Phe	Gln	Gly	Asp	Ser	Thr	Val	Thr	Lys	Ser	Cys	Ala	Ser
			65						70					75
Lys	Cys	Lys	Pro	Ser	Asp	Val	Asp	Gly	Ile	Gly	Gln	Thr	Leu	Pro
			80						85					90
Val	Ser	Cys	Cys	Asn	Thr	Glu	Leu	Cys	Asn	Val	Asp	Gly	Ala	Pro
			95						100					105
Ala	Leu	Asn	Ser	Leu	His	Cys	Gly	Ala	Leu	Thr	Leu	Leu	Pro	Leu
			110						115					120
Leu	Ser	Leu	Arg	Leu										
			125											

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100
attttctctt tctttctccc tcttgagtc ttctgagatg atggctcttg 150
gcgcagcggg agctaccogg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgcgg gaatectgta cccgggcggg 350
 aataagtacc agaccattga caactaccag ccgtaccctg gcgcagagga 400
 cgaggagtgc ggactgatg agtactgcgc tagtcccacc cgcggagggg 450
 acgcaggcgt gcaaatctgt ctgcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
 tctgggtcaa gatctgtaaa cctgtcctga aagaaggcca agtgtgtacc 800
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900
 gtaattcttc taggttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100
 ttatggaact cccctgtgat tgcagtaaat tactgtattg taaattctca 1150
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200
 ggtgctgcac tgcctatttt tcctcttggt atgtaaattt ttgtacacat 1250
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaatca 1300
 tttcagctta tagttcttaa aagcataacc ctttacccca ttttaattcta 1350
 gagtctagaa cgcaaggatc tcttggaatg acaaagata ggtacctaaa 1400
 atgtaacatg aaaatactag cttatcttct gaaatgtact atcttaatgc 1450
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 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala	
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser	
				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
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ttttgcagcg gaacgggaag gttttgtggg acccaggttg aaatgacggt 100
catttttttt tctttctcct tcnngagtcc ttntgagang atggtttttg 150
gcgagcgagg agctaaccgg gttttttgtn gcgatggtag cggcggtttt 200
cggcgggccac ctntgtctgg gagtgagcgc caccttgaat cggttttcaa 250
ttccaacgnt atcaagaacc tgccccacc gntgggcggc gctgcggggc 300
accaggnntt tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350
aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400
cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450
angcgggcgt gcaaatntgt ntngcctgca ggaagcgccg aaaacgctgc 500
atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

<400> 458
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ttctctcctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200
gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250
ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcaccct 300

tgaagtaatg tagacagaag ttctcaaatt tgcattattac atcaactgga 350
accagcagtg aatcttaaatg ttcacttaaa tcagaacttg cataagaaaag 400
agaatgggag tctgggtaaa taaagatgac tatatcagag acttgaaaag 450
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500
atcaggattt ttacagttha cttggagtgt ccaaaactgc aagcagtaga 550
gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600
aaaccgaat aaccctaatg cacatggcga ttttttaaaa ataaatagag 650
catatgaagt actcaaagat gaagatctac ggaaaaagta tgacaaatat 700
ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750
ctattatcgt tatgattttg gtatttatga tgatgatect gaaatcataa 800
cattggaaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850
tttgtaaatt ttactcccc aggctgttca cactgccatg atttagctcc 900
cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950
ctgttaactg tggatgatgat agaattgctt gccgaatgaa aggagtcaac 1000
agctatccca gtctcttcat ttttcggtct ggaatggccc cagtgaataa 1050
tcatggagac agatcaaagg agagttagt gagttttgca atgcagcatg 1100
ttagaagtac agtgacagaa ctttggacag gaaattttgt caactccata 1150
caaactgctt ttgctgctgg tattggctgg ctgatcactt tttgttcaa 1200
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aatcttccag attttgaact actttcgga aacacactag aggatcgttt 1350
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caaatgatcc tgagctgaaa aaactaaaaa ctctacttaa aaatgatcat 1450
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tctgtatgtt tttcagccgt ctctagcagt atttaaagga caaggaacca 1550
aagaatatga aattcatcat ggaaagaaga ttctatatga tatacttgcc 1600
tttgccaaaag aaagtgtgaa ttctcatgtt accacgcttg gacctcaaaa 1650
ttttcctgcc aatgacaaaag aaccatggct tggtgatttc tttgccccct 1700
ggtgtccacc atgtcgagct ttactaccag agttacgaag agcatcaaat 1750

cttcttttatg gtcagcttaa gtttggtaca ctagattgta cagttcatga 1800
gggactctgt aacatgtata acattcaggc ttatccaaca acagtgggtat 1850
tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900
atcttggagt tcatagagga tcttatgaat ccttcagtgg tctcccttac 1950
accaccacc ttcaacgaac tagttacaca aagaaaacac aacgaagtct 2000
ggatgggtga tttctattct ccgtgggtgtc atccttgcca agtcttaatg 2050
ccagaatgga aaagaatggc ccggacatta actggactga tcaacgtggg 2100
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cagtatcaca gttacaatgg ttggaatagg gatgcttatt ccctgagaat 2250
ctgggggtcta ggatttttac ctcaagtatc cacagatcta acacctcaga 2300
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cttggttagg atgattaaag gaaaagtgaag agctggaaaa gtagactgtc 2450
aggcttatgc tcagacatgc cagaaagctg ggatcagggc ctatccaact 2500
gttaagtttt atttctacga aagagcaaag agaaattttc aagaagagca 2550
gataaatacc agagatgcaa aagcaatgc tgccttaata agtgaaaaat 2600
tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650
tggtgaagat gaagaaaaag tttaaaagaa attctgacag atgacatcag 2700
aagacacctt tttagaatgt tacatttatg atgggaatga atgaacatta 2750
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agaagggtct gcaaactttt tctgtaaagg gccggtttat aaatatttta 2850
gactttgcag gctataatat atgggtcaca catgagaaca agaataagagt 2900
catcatgtat tctttgttat ttgcttttaa caacctttaa aaaatattaa 2950
aacgattctt agctcagagc catacaaaag taggctggat tcagtcctatg 3000
gaccatagat tgctgtcccc ctgcacggac ttataatgtt tcaggtggct 3050
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 ttatgctgta ttattatgag gagattcttc attgttttct ttccttctca 3300
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 tagagttcta tattttaaag atatatgtgt tcatgtattt tctgaaattg 3550
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 aatgatactg tagttattcc agttactagt ttactgtcag agggctgcct 3800
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 ctcaaagaat cacaatttg tcagtaacat gtagttgttt agttataatt 3950
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 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys
1				5					10				15	
Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp Phe Leu Lys	Ile Asn Arg Ala Tyr	Glu Val Leu Lys Asp	Glu
	80	85	90
Asp Leu Arg Lys	Lys Tyr Asp Lys Tyr	Gly Glu Lys Gly Leu	Glu
	95	100	105
Asp Asn Gln Gly	Gly Gln Tyr Glu Ser	Trp Asn Tyr Tyr Arg	Tyr
	110	115	120
Asp Phe Gly Ile	Tyr Asp Asp Asp Pro	Glu Ile Ile Thr Leu	Glu
	125	130	135
Arg Arg Glu Phe	Asp Ala Ala Val Asn	Ser Gly Glu Leu Trp	Phe
	140	145	150
Val Asn Phe Tyr	Ser Pro Gly Cys Ser	His Cys His Asp Leu	Ala
	155	160	165
Pro Thr Trp Arg	Asp Phe Ala Lys Glu	Val Asp Gly Leu Leu	Arg
	170	175	180
Ile Gly Ala Val	Asn Cys Gly Asp Asp	Arg Met Leu Cys Arg	Met
	185	190	195
Lys Gly Val Asn	Ser Tyr Pro Ser Leu	Phe Ile Phe Arg Ser	Gly
	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser	Leu
	215	220	225
Val Ser Phe Ala	Met Gln His Val Arg	Ser Thr Val Thr Glu	Leu
	230	235	240
Trp Thr Gly Asn	Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala	Ala
	245	250	255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp	Cys
	260	265	270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe	Leu
	275	280	285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr	Leu Glu Val Ile His	Asn
	290	295	300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp	Arg
	305	310	315
Leu Ala His His	Arg Trp Leu Leu Phe	Phe His Phe Gly Lys	Asn
	320	325	330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu	Leu
	335	340	345
Lys Asn Asp His	Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser	Ala
	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
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<210> 461
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<220>
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<400> 461
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<210> 462
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<220>
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<400> 462
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<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

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<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

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Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg	20	25	30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly				

	155		160		165
His Ile Val Thr	Val Ala Ser Val Cys Gly	His Glu Gly Ile Pro			
	170	175		180	
Tyr Leu Ile Pro	Tyr Cys Ser Ser Lys Phe	Ala Ala Val Gly Phe			
	185	190		195	
His Arg Gly Leu	Thr Ser Glu Leu Gln	Ala Leu Gly Lys Thr Gly			
	200	205		210	
Ile Lys Thr Ser	Cys Leu Cys Pro Val	Phe Val Asn Thr Gly Phe			
	215	220		225	
Thr Lys Asn Pro	Ser Thr Arg Leu Trp	Pro Val Leu Glu Thr Asp			
	230	235		240	
Glu Val Val Arg	Ser Leu Ile Asp Gly	Ile Leu Thr Asn Lys Lys			
	245	250		255	
Met Ile Phe Val	Pro Ser Tyr Ile Asn	Ile Phe Leu Arg Leu Gln			
	260	265		270	
Lys Phe Leu Pro	Glu Arg Ala Ser Ala	Ile Leu Asn Arg Met Gln			
	275	280		285	
Asn Ile Gln Phe	Glu Ala Val Val Gly	His Lys Ile Lys Met Lys			
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<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20						25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50						55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser		65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln		80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp		95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln		110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser		125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro		140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala		155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg		170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro		185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala		200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys		215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys		230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe		245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe		260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro		275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe		290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu		305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His		320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu		335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
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Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
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<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
 50 55 60
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
 65 70 75
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
 80 85 90
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
 95 100 105
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
 110 115 120
 Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
 125 130 135
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
 140 145 150
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
 155 160 165
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
 170 175 180
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
 185 190 195
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met
 200 205 210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
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Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

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<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

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Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu	50	55	60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn	65	70	75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu	80	85	90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile	95	100	105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg	110	115	120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp	125	130	135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg	140	145	150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln	155	160	165
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<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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 gattttcctt cagtgatgtg cttttgtga aagaattaat gaactccagt 2250
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300
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 agggaggcta atttcttt 2368

<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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			20						25					30
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
			35						40					45
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
			50						55					60
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
			65						70					75
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
			80						85					90
Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
			95						100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
			110						115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
			125						130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
			140						145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
			155						160					165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr
170 175 180

Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala
185 190 195

Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile
200 205 210

Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg
215 220 225

Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln
230 235 240

Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu
245 250 255

Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu
260 265 270

Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu
275 280 285

Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly
290 295 300

Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu
305 310 315

Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr
320 325 330

Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala
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Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

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<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 474

ctctctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser	170	175	180	
Val	Ile	Tyr	Asp	Gln	Leu	Cys	Ser	Val	Pro	Ser	Tyr	Ser	Ile	Cys	185	190	195	
Glu	Lys	Lys	Phe	Ser	Met	200												

<210> 478

<211> 27
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
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<210> 479
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 479
acaagtgtct tcccaacctg 20

<210> 480
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<212> DNA
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<220>
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<400> 480
atcctcccag agccatggta cctc 24

<210> 481
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<212> DNA
<213> Homo sapiens

<400> 482
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<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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			20						25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
			35						40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
			50						55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
			65						70					75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
			80						85					90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val
380	385 390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu
395	400 405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val
410	415 420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg
425	430 435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu
440	445 450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro
455	460 465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile
470	475 480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu
485	490 495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr
500	505 510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly
515	520 525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp
530	535 540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly
545	550 555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser
560	565 570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn
575	580 585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg
590	595 600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu
605	610 615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe
620	625 630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile
635	640 645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser
650	655 660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

ggcattggag cagtgcctgg tg 22

<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

tgagggccta gatgcggctg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 492

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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 493

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<210> 494

<211> 20

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

<210> 497
<211> 4199
<212> DNA
<213> Homo sapiens

<400> 497
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His	440	445	450
Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser	455	460	465
Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala	470	475	480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu	515	520	525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr	Asn Asn
	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	
	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp
	635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu
	650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn	Met
	665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu
	680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp
	695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser
	710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu	Val
	725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr
	740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser
	755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile
	770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys	Ile
	785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg
	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
Asp Ser Ile Lys Gln Tyr	1040		

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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taaagaccca gctgtgaccg 20

<210> 500
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<220>
<223> Synthetic oligonucleotide probe

<400> 500
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<210> 501
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<212> DNA
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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

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<210> 503
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 503
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<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu				

	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys Gly				
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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ctgctgcctg acccccagca caataaaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

tggagcagca atatgccagc c 21

<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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agttgggtct ccgtgtttca ggccggctcc cctttcctgg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250
ggacttttga tgatgtttga cccagcggca ggaatagcag gcaacgtgat 300
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atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305		310		315
Glu Thr Ser Ser	Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu				
	320		325		330
His Leu Asn Ser	Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu				
	335		340		345
Glu Met Pro Pro	Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala				
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Glu Ala Glu Lys

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcacctt ttntctctcc cncctcaca tctatgtctt cgccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 517
 caacgtgatt tcaaagctgg gctc 24

<210> 518
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatgggtg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg ccggtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcacccgggt ggctgggcta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450
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 aaacgtgaaa taaaaagagc aaaaaaaaa 1679

<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
				140					145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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<212> PRT

<213> Homo sapiens

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Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp	80	85	90
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Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp	110	115	120
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Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu	140	145	150
Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro	155	160	165
Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly	170	175	180
Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala	185	190	195
Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala	200	205	210
Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser	215	220	225
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Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val	275	280	285
Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met	290	295	300
Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu	305	310	315
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Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala	410	415	420
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Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val	560	565	570
Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu	575	580	585
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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val	695	700	705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly	710	715	720
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Trp

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<211> 4308

<212> DNA

<213> Homo sapiens

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<221> unsure

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<223> unknown base

<400> 527

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<213> Homo sapiens

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<212> DNA

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<211> 352

<212> PRT

<213> Homo Sapien

<400> 612

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Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu		
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe		
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Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln		
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Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro		
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245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile		
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Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr		
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Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys		
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 gcgtctgacc cggaaccct ttcacttctc tgctcccgag gtgtcctcgg 1700
 gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaac 1750
 tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

Met	Arg	Asn	Lys	Lys	Ile	Leu	Lys	Glu	Asp	Glu	Leu	Leu	Ser	Glu
1				5					10					15

Thr	Gln	Gln	Ala	Ala	Phe	His	Gln	Ile	Ala	Met	Glu	Pro	Phe	Glu
				20					25					30

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser
				35					40					45

Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala
				50					55					60

Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg
				65					70					75

Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp
				80					85					90

Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His
				95					100					105

Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu
				110					115					120

Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp
				125					130					135

Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln
				140					145					150

Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro
				155					160					165

Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys
				170					175					180

Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

185					190					195				
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln
				200										210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln
				215										225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys
				230										240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro
				245										255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met
				260										270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro
				275										285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln
				290										300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val
				305										315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro
				320										330
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr
				335										345
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln
				350										360
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys
				365										375
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro
				380										390
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser
				395										405
Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn
				410										420
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala
				425										435
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu
				440										450
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr
				455										465
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
 cccacgcgtc cgaaggcaga caaaggttca tttgtaaaga agtccttcc 50
 agcacctect ctcttctcct tttgccc aaa ctcacccagt gagtgtgagc 100
 atttaagaag catcctctgc caagaccaa aggaaagaag aaaaagggcc 150
 aaaagccaaa atgaaactga tggtaactgt tttcaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atcgctctc ttgctacaga 250
 aagatactaa aagatcaca ctgtcacaac cttccggaag gagtagctga 300
 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgccc 400
 aaagacgttt tctttggacc aaagatctct ttogtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaattctgt 600
 gttaaacaag tagtaataaa agttaattca atctaaaaa aaaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
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 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100
 accccgccgt ggtggttga gggcgcgag tagagcagca gcacaggcgc 150
 ggggtcccggt aggcgcgtc tgctcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgc cgcgcgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg ctctctcttc 300
 ggggtggtta taaaatctc caatgaagct actaacatta ctccaaagca 350
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 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaaatt tcaatcccag tggaaagaat ttggcctgga 500
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550
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 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650
 tattgtacca ctttctcagt ctttctctcc tcaaggaatg ccagagggcg 700
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cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050
ccaagtattc ctgttcattc aattggatac tatgatgcac agaagctcct 1100
agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150
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caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300
ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgacctcag 1350
agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400
aaaggaaggg tggagacctc gaagaacaat tttgtttgca agctgggatg 1450
cagaagaatt tggctctctt ggttctactg agtgggcaga ggagaattca 1500
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acctcactgt ggeccagggt cgaggaggga tgggtgttga gctagccaat 1950
tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000
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acagaaattg cttccaagtt cagtgaaga ctccaggact ttgacaaaag 2150
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gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300
aggaatttat gatgctctgt ttgatattga aagcaaagtg gaccttcca 2350
aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagt 2400

caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450
 gaatccgtat tgaatttgtg tggatatgtca ctcagaaaga atcgtaatgg 2500
 gtatatgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550
 atatataa 2558

<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618
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 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
 20 25 30
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90
 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
 95 100 105
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
 110 115 120
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
 125 130 135
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
 140 145 150
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
 155 160 165
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
 170 175 180
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
 185 190 195
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
 200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met Pro	500	505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn Asp	Phe Glu Val Phe Phe	515	520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg Ala	Arg Tyr Thr Lys Asn	530	535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr Pro	Leu Tyr His Ser Val	545	550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys Phe	Tyr Asp Pro Met Phe	560	565	570
Lys Tyr His Leu	Thr Val Ala Gln Val Arg	Gly Gly Met Val Phe	575	580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro Phe	Asp Cys Arg Asp Tyr	590	595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp Lys	Ile Tyr Ser Ile Ser	605	610	615
Met Lys His Pro	Gln Glu Met Lys Thr Tyr	Ser Val Ser Phe Asp	620	625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe Thr	Glu Ile Ala Ser Lys	635	640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp Lys	Ser Asn Pro Ile Val	650	655	660
Leu Arg Met Met	Asn Asp Gln Leu Met Phe	Leu Glu Arg Ala Phe	665	670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg Pro	Phe Tyr Arg His Val	680	685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys Tyr	Ala Gly Glu Ser Phe	695	700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp Ile	Glu Ser Lys Val Asp	710	715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys Arg	Gln Ile Tyr Val Ala	725	730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu Thr	Leu Ser Glu Val Ala	740	745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50